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<p>(21) International Application Number: PCT/US00/01979</p> <p>(22) International Filing Date: 28 January 2000 (28.01.00)</p> <p>(30) Priority Data: 60/118,381 29 January 1999 (29.01.99) US</p> <p>(71) Applicants: UNIVERSITY OF UTAH RESEARCH FOUNDATION [US/US]; Suite 110, 615 Arapeen Drive, Salt Lake City, UT 84108 (US). COGNETIX, INC. [US/US]; Suite 201, 421 Wakara Way, Salt Lake City, UT 84108 (US).</p> <p>(72) Inventors: WATKINS, Maren; 845 East Garfield Avenue, Salt Lake City, UT 84105 (US). OLIVERA, Baldomero, M.; 1370 Bryan Avenue, Salt Lake City, UT 84108 (US). HILLYARD, David, R.; 3685 Juno Circle, Salt Lake City, UT 84124 (US). MCINTOSH, J., Michael; 1151 South 2000 East, Salt Lake City, UT 84108 (US). JONES, Robert, M.; 44 West Broadway #2103 South, Salt Lake City, UT 84101 (US).</p> <p>(74) Agents: IHNEN, Jeffrey, L. et al.; Rothwell, Figg, Ernst & Kurz, Suite 701 East, 555 13th Street N.W., Columbia Square, Washington, DC 20004 (US).</p>		<p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>	
<p>(54) Title: ALPHA-CONOTOXIN PEPTIDES</p> <p>(57) Abstract</p> <p>The invention relates to relatively short peptides (termed α-conotoxins herein), about 10–30 residues in length, which are naturally available in minute amounts in the venom of the cone snails or analogous to the naturally available peptides, and which preferably include two disulfide bonds.</p>			

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TITLE OF THE INVENTION

ALPHA-CONOTOXIN PEPTIDES

This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

The invention relates to relatively short peptides (termed α -conotoxins herein), about 10-30 residues in length, which are naturally available in minute amounts in the venom of the cone snails or analogous to the naturally available peptides, and which preferably include two disulfide bonds.

The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

The predatory cone snails (*Conus*) have developed a unique biological strategy. Their venom contains relatively small peptides that are targeted to various neuromuscular receptors and may be equivalent in their pharmacological diversity to the alkaloids of plants or secondary metabolites of microorganisms. Many of these peptides are among the smallest nucleic acid-encoded translation products having defined conformations, and as such, they are somewhat unusual. Peptides in this size range normally equilibrate among many conformations. Proteins having a fixed conformation are generally much larger.

The cone snails that produce these peptides are a large genus of venomous gastropods comprising approximately 500 species. All cone snail species are predators that inject venom to capture prey, and the spectrum of animals that the genus as a whole can envenomate is broad. A wide variety of hunting strategies are used, however, every *Conus* species uses fundamentally the same basic pattern of envenomation.

Several peptides isolated from *Conus* venoms have been characterized. These include the α -, μ - and ω -conotoxins which target nicotinic acetylcholine receptors, muscle sodium channels,

and neuronal calcium channels, respectively (Olivera et al., 1985). Conopressins, which are vasopressin analogs, have also been identified (Cruz et al., 1987). In addition, peptides named conantokins have been isolated from *Conus geographus* and *Conus tulipa* (Mena et al., 1990; Haack et al., 1990).

5 The α -conotoxins are small peptides highly specific for neuromuscular junction nicotinic acetylcholine receptors (Gray et al., 1981; Marshall and Harvey, 1990; Blount et al., 1992; Jacobsen et al., 1997) or highly specific for neuronal nicotinic acetylcholine receptors (Fainzilber et al., 1994; Johnson et al., 1995; Cartier et al., 1996; Luo et al., 1998). The α -conotoxins with specificity for neuromuscular junction nicotinic acetylcholine receptors are used as neuromuscular blocking agents
10 for use in conjunction with surgery, as disclosed in U.S. patent application Serial No. 09/_____, filed 21 January 2000 (Attorney Docket No. 2314-178.A) and international patent application No. PCT/US00/_____, filed 21 January 2000 (Attorney Docket No. 2314-138.PCT), each incorporated by reference herein. Additional α -conotoxins and uses for them have been described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,432,155; 5,514,774, each incorporated herein by reference.

15 Additional uses for α -conotoxins are described in U.S. Serial No. 09/219,446, filed 22 December 1998, incorporated herein by reference. In this application, α -conotoxins with specificity for neuronal nicotinic acetylcholine receptors are used for treating disorders regulated at neuronal nicotinic acetylcholine receptors. Such disorders include, but are not limited to, cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders (such
20 as bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder) and small cell lung carcinoma, as well as the localization of small cell lung carcinoma.

It is desired to provide additional α -conotoxin peptides having uses as described herein.

SUMMARY OF THE INVENTION

The invention relates to relatively short peptides (termed α -conotoxins herein), about 10-30 residues in length, which are naturally available in minute amounts in the venom of the cone snails or analogous to the naturally available peptides, and which preferably include two disulfide bonds.
25

More specifically, the present invention is directed to α -conotoxin peptides having the general formula I:

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Cys-Cys-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Cys-Xaa₁₀-Xaa₁₁-Xaa₁₂-Cys-Xaa₁₃ (SEQ ID NO1:), wherein Xaa₁ is des-Xaa₁, Ile, Leu or Val; Xaa₂ is des-Xaa₂, Ala or Gly; Xaa₃ is des-Xaa₃, Gly, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa₄ is des-

Xaa₁, Asp, Phe, Gly, Ala, Glu, γ -carboxy-Glu (Gla) or any unnatural aromatic amino acid; Xaa₂ is Glu, Gla, Asp, Ala, Thr, Ser, Gly, Ile, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₃ is Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₄ is Asp, Glu, Gla, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₅ is Ser, Thr, Asn, Ala, Gly, His, halo-His, Pro or hydroxy-Pro; Xaa₆ is Thr, Ser, Ala, Asp, Asn, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₀ is Gly, Ser, Thr, Ala, Asn, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₁ is Gln, Leu, His, halo-His, Trp (D or L), halo-Trp, neo-Trp, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa₁₂ is Asn, His, halo-His, Ile, Leu, Val, Gln, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₃ is des-Xaa₁₃, Val, Ile, Leu, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid. The C-terminus may contain a free carboxyl group or an amide group. The halo is chlorine, bromine or iodine, preferably iodine for Tyr and His and preferably bromine for Trp. The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

More specifically, the present invention is directed to α -conotoxin peptides having the general formula II:

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Cys-Cys-Xaa₅-Xaa₆-Xaa₇-Xaa₈-Cys-Xaa₉-Xaa₁₀-Xaa₁₁-Xaa₁₂-Xaa₁₃-Xaa₁₄-Cys-Xaa₁₅-Xaa₁₆-Xaa₁₇ (SEQ ID NO:2), wherein Xaa₁ is des-Xaa₁, Asp, Glu or γ -carboxy-Glu (Gla); Xaa₂ is des-Xaa₂, Gln, Ala, Asp, Glu, Gla; Xaa₃ is des-Xaa₃, Gly, Ala, Asp, Glu, Gla, Pro or hydroxy-Pro; Xaa₄ is des-Xaa₄, Gly, Glu, Gla, Gln, Asp, Asn, Pro or hydroxy-Pro; Xaa₅ is Ser, Thr, Gly, Glu, Gla, Asn, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing

amino acid; Xaa₆ is Asp, Asn, His, halo-His, Thr, Ser, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₇ is Pro or hydroxy-Pro; Xaa₈ is Ala, Ser, Thr, Asp, Val, Ile, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing 5 amino acid; Xaa₉ is Gly, Ile, Leu, Val, Ala, Thr, Ser, Pro, hydroxy-Pro, Phe, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa₁₀ is Ala, Asn, Phe, Pro, hydroxy-Pro, Glu, Gla, Gln, His, halo-His, Val, Ser, Thr, Arg, ornithine, homoarginine, Lys, 10 N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₁ is Thr, Ser, His, halo-His, Leu, Ile, Val, Asn, Met, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, 15 nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₂ is Asn, Pro, hydroxy-Pro, Gln, Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or 20 any unnatural hydroxy containing amino acid; Xaa₁₃ is des-Xaa₁₃, Gly, Thr, Ser, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₄ is des-Xaa₁₄, Ile, Val, Asp, Leu, Phe, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic 25 amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; and Xaa₁₅ is des-Xaa₁₅, Gly, Ala, Met, Ser, Thr, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₆ is des-Xaa₁₆, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic 30 amino acid; Xaa₁₇ is des-Xaa₁₇, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid. The C-terminus may contain a free carboxyl group or an amide group. The halo is preferably bromine, chlorine or iodine, more preferably iodine for His or Tyr and bromine for Trp. The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-

phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

More specifically, the present invention is directed to α -conotoxin peptides having the general formula III:

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Cys-Cys-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Cys-Xaa₁₀-Xaa₁₁-Xaa₁₂-Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Cys-Xaa₁₇-Xaa₁₈-Xaa₁₉-Xaa₂₀-Xaa₂₁-Xaa₂₂-Xaa₂₃-Xaa₂₄ (SEQ ID NO:3), wherein Xaa₁ is des-Xaa₁, Ser or Thr; Xaa₂ is des-Xaa₂, Asp, Glu, γ -carboxy-Glu (Gla), Asn, Ser or Thr; Xaa₃ is des-Xaa₃, Ala, Gly, Asn, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₄ is des-Xaa₄, Ala, Val, Leu, Ile, Gly, Glu, Gla, Gln, Asp, Asn, Phe, Pro, hydroxy-Pro or any unnatural aromatic amino acid; Xaa₅ is des-Xaa₅, Thr, Ser, Asp, Glu, Gla, Gln, Gly, Val, Asp, Asn, Ala, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₆ is Thr, Ser, Asp, Asn, Met, Val, Ala, Gly, Leu, Ile, Phe, any unnatural aromatic amino acid, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₇ is Ile, Leu, Val, Ser, Thr, Gln, Asn, Asp, Arg, His, halo-His, Phe, any unnatural aromatic amino acid, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₈ is Pro, hydroxy-Pro, Ser, Thr, Ile, Asp, Leu, Val, Gly, Ala, Phe, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₉ is Val, Ala, Gly, Ile, Leu, Asp, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₀ is His, halo-His, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Asn, Ala, Ser, Thr, Phe, Ile, Leu, Gly, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₁ is Leu, Gln, Val, Ile, Gly, Met, Ala, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Ser, Thr, Arg, homoarginine, ornithine, any unnatural basic amino acid, Asn, Glu, Gla, Gln, Phe, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa₁₂ is Glu, Gla, Gln, Asn, Asp, Pro, hydroxy-Pro, Ser, Gly, Thr, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Arg, homoarginine, ornithine, any unnatural basic amino acid, Phe, His, halo-

His, any unnatural aromatic amino acid, Leu, Met, Gly, Ala, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₃ is His, halo-His, Asn, Thr, Ser, Ile, Val, Leu, Phe, any unnatural aromatic amino acid, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Try, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₄ is Ser, Thr, Ala, Gln, Pro, hydroxy-Pro, Gly, Ile, Leu, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₅ is Asn, Glu, Gla, Asp, Gly, His, halo-His, Ala, Leu, Gln, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₆ is Met, Ile, Thr, Ser, Val, Leu, Pro, hydroxy-Pro, Phe, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, any unnatural hydroxy containing amino acid, Glu, Gla, Ala, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₇ is des-Xaa₁₇, Gly, Asp, Asn, Ala, Ile, Leu, Ser, Thr, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₈ is des-Xaa₁₈, Gly, Glu, Gla, Gln, Trp (D or L), neo, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₉ is des-Xaa₁₉, Ser, Thr, Val, Ile, Ala, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₀ is des-Xaa₂₀, Val, Asp, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₁ is des-Xaa₂₁, Asn, Pro or hydroxy-Pro; Xaa₂₂ is des-Xaa₂₂, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₃ is des-Xaa₂₃, Ser or Thr; Xaa₂₄ is des-Xaa₂₄, Leu, Ile or Val; with the proviso that (a) Xaa₁ is not Gly, when Xaa₁ is des-Xaa₁, Xaa₂ is des-Xaa₂, Xaa₃ is des-Xaa₃, Xaa₄ is des-Xaa₄, Xaa₅ is Ser, Xaa₆ is His, Xaa₇ is Pro, Xaa₈ is Ala, Xaa₁₀ is Ser, Xaa₁₁ is Val, Xaa₁₂ is Asn, Xaa₁₃ is Asn, Xaa₁₄ is Pro, Xaa₁₅ is Asp, Xaa₁₆ is Ile, Xaa₁₇ is des-Xaa₁₇, Xaa₁₈ is des-Xaa₁₈, Xaa₁₉ is des-Xaa₁₉, Xaa₂₀ is des-Xaa₂₀, Xaa₂₁ is des-Xaa₂₁, Xaa₂₂ is des-Xaa₂₂, Xaa₂₃ is des-Xaa₂₃, and Xaa₂₄ is des-Xaa₂₄. The C-terminus may contain a free carboxyl group or an amide group. The halo is preferably bromine, chlorine or iodine, more preferably iodine for His and Tyr and bromine for Trp. The Cys residues may be in D or L configuration and may

optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

5 The present invention is also directed to novel specific α -conotoxin peptides of general formula I having the formulas:

Asp-Xaa₁-Cys-Cys-Ser-Asp-Ser-Arg-Cys-Gly-Xaa₂-Asn-Cys-Leu (SEQ ID NO:4);
Ala-Cys-Cys-Ser-Asp-Arg-Arg-Cys-Arg-Xaa₃-Arg-Cys (SEQ ID NO:5);
Phe-Thr-Cys-Cys-Arg-Arg-Gly-Thr-Cys-Ser-Gln-His-Cys (SEQ ID NO:6);
10 Asp-Xaa₄-Cys-Cys-Arg-Arg-His-Ala-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:7);
Asp-Xaa₄-Cys-Cys-Arg-Xaa₅-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:8);
Gly-Cys-Cys-Ser-Asp-Xaa₆-Arg-Cys-Arg-Xaa₇-Arg-Cys-Arg (SEQ ID NO:9);
Gly-Gly-Cys-Cys-Ser-Asp-Xaa₈-Arg-Cys-Ala-Xaa₉-Arg-Cys (SEQ ID NO:10);
Ile-Ala-Xaa₁₀-Asp-Ile-Cys-Cys-Ser-Xaa₁₁-Xaa₁₂-Asp-Cys-Asn-His-Xaa₁₃-Cys-Val (SEQ ID
15 NO:11); and

Gly-Cys-Cys-Ser-Asp-Xaa₁₄-Arg-Cys-Xaa₁₅-His-Gln-Cys (SEQ ID NO:12),

wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group. The halo is preferably bromine, chlorine or iodine, more preferably iodine for Tyr and bromine for Trp. In addition, the His residues may be substituted with halo-His; the Arg residues may be substituted by Lys, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Tyr residues may be substituted with any unnatural hydroxy containing amino acid; the Ser residues may be substituted with Thr; the Thr residues may be substituted with Ser; and the Phe and Trp residues may be substituted with any unnatural aromatic amino acid. The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

More specifically, the present invention is directed to the following α -conotoxin peptides of general formula I:

- 5 Im1.1: SEQ ID NO:4, wherein Xaa₁ is Glu and Xaa₂ is Lys;
 Im1.2: SEQ ID NO:5, wherein Xaa₃ is Trp;
Rg1.2: SEQ ID NO:6;
Rg1.6: SEQ ID NO:7, wherein Xaa₄ is Tyr;
Rg1.6A: SEQ ID NO:8, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
Rg1.7: SEQ ID NO:9, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
Rg1.9: SEQ ID NO:10, wherein Xaa₃ is Trp and Xaa₅ is Pro;
10 Rg1.10: SEQ ID NO:11, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp and Xaa₅ is Pro; and
 Rg1.11: SEQ ID NO:12, wherein Xaa₂ is Lys and Xaa₅ is Pro.

The C-terminus of Im1.1, Rg1.7 and Rg1.10 preferably contains a free carboxyl group. The C-terminus of Im1.2, Rg1.2, Rg1.6, Rg1.6A, Rg1.9 and Rg1.11 preferably contains an amide group.

15 The present invention is further directed to novel specific α -conotoxin peptides of general formula II having the formulas:

- Cys-Cys-Ser-Asp-Xaa₁-Ala-Cys-Xaa₂-Gln-Thr-Xaa₃-Gly-Cys-Arg (SEQ ID NO:13);
Cys-Cys-Xaa₁-Asn-Xaa₃-Ala-Cys-Arg-His-Thr-Gln-Gly-Cys (SEQ ID NO:14);
Gly-Cys-Cys-Xaa₃-His-Xaa₅-Ala-Cys-Gly-Arg-His-Xaa₄-Cys (SEQ ID NO:15);
20 Ala-Xaa₁-Cys-Cys-Asn-Asn-Xaa₃-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:16);
Ala-Xaa₁-Gly-Cys-Cys-Asn-Asn-Xaa₃-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:17);
Xaa₅-Xaa₃-Cys-Cys-Asn-Asn-Xaa₃-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:18);
Asp-Xaa₁-Asn-Cys-Cys-Xaa₃-Asn-Xaa₅-Ser-Cys-Xaa₂-Arg-Xaa₃-Arg-Cys-Thr (SEQ ID NO:19);
25 Gly-Cys-Cys-Ser-Thr-Xaa₁-Xaa₃-Cys-Ala-Val-Leu-Xaa₄-Cys (SEQ ID NO:20);
Gly-Cys-Cys-Gly-Asn-Xaa₃-Asp-Cys-Thr-Ser-His-Ser-Cys (SEQ ID NO:21);
Gly-Cys-Cys-Ser-Asn-Xaa₁-Xaa₃-Cys-Ala-His-Asn-Asn-Xaa₅-Asp-Cys-Arg (SEQ ID NO:42);
Gly-Cys-Cys-Xaa₄-Asn-Xaa₃-Val-Cys-Xaa₂-Xaa₂-Xaa₄-Cys-Xaa₃-Xaa₂ (SEQ ID NO:154);
30 Xaa₆-Xaa₁-Xaa₃-Gly-Cys-Cys-Arg-His-Xaa₅-Ala-Cys-Gly-Xaa₂-Asn-Arg-Cys (SEQ ID NO:155);

Cys-Cys-Ala-Asp-Xaa₁-Asp-Cys-Arg-Phe-Arg-Xaa₁-Gly-Cys (SEQ ID NO:156);
Gly-Cys-Cys-Xaa₄-Asn-Xaa₁-Ser-Cys-Xaa₁-Xaa₂-Thr-Xaa₄-Cys-Ser-Xaa₃-Xaa₂ (SEQ
ID NO:157);
Cys-Cys-Ser-Asn-Xaa₁-Thr-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:158);
5 Cys-Cys-Ala-Asn-Xaa₁-Ile-Cys-Xaa₂-Asn-Thr-Xaa₁-Gly-Cys (SEQ ID NO:159);
Cys-Cys-Asn-Asn-Xaa₁-Thr-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:160);
Cys-Cys-Ser-Asn-Xaa₁-Val-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:161);
Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₁-Xaa₂-Cys-Ile-Ala-Ser-Asn-Xaa₃-Xaa₂-Cys-Gly (SEQ ID
NO:162);
10 Gly-Cys-Cys-Ser-His-Xaa₁-Val-Cys-Ser-Ala-Met-Ser-Xaa₃-Ile-Cys (SEQ ID NO:163);
Gly-Cys-Cys-Xaa₁-Asn-Xaa₅-Xaa₄-Cys-Gly-Ala-Ser-Xaa₂-Thr-Xaa₄-Cys (SEQ ID NO:164);
Gly-Cys-Cys-Ser-Xaa₄-Xaa₁-Xaa₂-Cys-Phe-Ala-Thr-Asn-Xaa₃-Asp-Cys (SEQ ID NO:165);
Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₁-Xaa₂-Cys-Ile-Ala-Asn-Asn-Xaa₃-Leu-Cys-Ala (SEQ ID
NO:166);
15 Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₁-Xaa₂-Cys-Ile-Ala-Asn-Asn-Xaa₃-Phe-Cys-Ala (SEQ ID
NO:167);
Asp-Cys-Cys-Ser-Asn-Xaa₁-Xaa₂-Cys-Ser-Gln-Asn-Asn-Xaa₃-Asp-Cys-Met (SEQ ID
NO:168); and
Asp-Cys-Cys-Ser-Asn-Xaa₁-Xaa₂-Cys-Ala-His-Asn-Asn-Xaa₃-Asp-Cys-Arg (SEQ ID
20 NO:169),
wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or
N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr, mono-halo-
Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and
the C-terminus contains a carboxyl or amide group. The halo is preferably bromine, chlorine or
25 iodine, more preferably iodine for Tyr and bromine for Trp. In addition, the His residues may be
substituted with halo-His; the Arg residues may be substituted by Lys, ornithine, homoarginine, N-
methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Lys
residues may be substituted by Arg, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Tyr residues may be substituted with
30 any unnatural hydroxy containing amino acid; the Ser residues may be substituted with Thr; the Thr
residues may be substituted with Ser; and the Phe and Trp residues may be substituted with any
unnatural aromatic amino acid. The Cys residues may be in D or L configuration and may

optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

5 More specifically, the present invention is directed to the following α -conotoxin peptides of general formula II:

- | | |
|--------|---|
| Sn1.1: | SEQ ID NO:13, wherein Xaa ₂ is Lys and Xaa ₅ is Pro; |
| Sn1.2: | SEQ ID NO:14, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Sl1.3: | SEQ ID NO:15, wherein Xaa ₃ is Trp, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| A1.2: | SEQ ID NO:16, wherein Xaa ₂ is Lys and Xaa ₅ is Pro; |
| Bu1.1: | SEQ ID NO:17, wherein Xaa ₂ is Lys and Xaa ₅ is Pro; |
| Bu1.2: | SEQ ID NO:18, wherein Xaa ₂ is Lys and Xaa ₅ is Pro; |
| Bu1.3: | SEQ ID NO:19, wherein Xaa ₁ is Glu, Xaa ₃ is Trp and Xaa ₅ is Pro; |
| Bu1.4: | SEQ ID NO:20, wherein Xaa ₄ is Tyr and Xaa ₅ is Pro ; |
| Cr1.3: | SEQ ID NO:21, wherein Xaa ₅ is Pro; |
| Di1.1: | SEQ ID NO:42 wherein Xaa ₅ is Pro; |
| Ms1.7: | SEQ ID NO:154, wherein Xaa ₂ is Lys, Xaa ₃ is Trp, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| P1.7: | SEQ ID NO:155, wherein Xaa ₁ is Glu, Xaa ₂ is Lys, Xaa ₅ is Pro and Xaa ₆ is Gln; |
| Ms1.2: | SEQ ID NO:156, wherein Xaa ₅ is Pro; |
| Ms1.3: | SEQ ID NO:157, wherein Xaa ₁ is Lys, Xaa ₃ is Trp, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| Ms1.4: | SEQ ID NO:158, wherein Xaa ₁ is Glu, Xaa ₂ is Lys, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| Ms1.5: | SEQ ID NO:159, wherein Xaa ₂ is Lys and Xaa ₅ is Pro; |
| Ms1.8: | SEQ ID NO:160, wherein Xaa ₁ is Glu, Xaa ₂ is Lys, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| Ms1.9: | SEQ ID NO:161, wherein Xaa ₁ is Glu, Xaa ₂ is Lys, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| Bt1.7: | SEQ ID NO:162, wherein Xaa ₂ is Lys, Xaa ₄ is Tyr and Xaa ₅ is Pro; |
| Lv1.5: | SEQ ID NO:163, wherein Xaa ₅ is Pro; |

- Ms1.10: SEQ ID NO:164, wherein Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;
Om1.1: SEQ ID NO:165, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
R1.6: SEQ ID NO:166, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
R1.7: SEQ ID NO:167, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
5 Vr1.1: SEQ ID NO:168, wherein Xaa₅ is Pro; and
Vr1.2: SEQ ID NO:169, wherein Xaa₅ is Pro.

The C-terminus preferably contains a carboxyl group for the peptides Sn1.1, Sn1.2, Cr1.3, Di1.1, Ms1.2, Ms1.4, Ms1.5, Ms1.8, Ms1.9, Vr1.1 and Vr1.2. The C-terminus of the other peptides preferably contains an amide group.

10 The present invention is also directed to novel specific α -conotoxin peptides of general formula III having the formulas:

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Leu-Xaa₁-His-Ser-Asn-Met-Cys (SEQ ID NO:22);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-Arg-Gln-Asn-Asn-Ala-Xaa₁-Xaa₄-Cys-Arg (SEQ ID NO:23);

15 Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₁-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:24);

Xaa₅-Xaa₁-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:25);

20 Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Asp (SEQ ID NO:26);

Xaa₅-Arg-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:27);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Gly-Ile-Cys-Arg (SEQ ID NO:28);

25 Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Thr-Cys-Arg (SEQ ID NO:29);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Val-Cys-Arg (SEQ ID NO:30);

30 Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Ile-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:31);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg-Arg-Arg (SEQ ID NO:32);

Gly-Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ala-Val-Asn-His-Xaa,-Xaa,-Leu-Cys (SEQ ID NO:33);

Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ser-Val-Asn-His-Xaa,-Xaa,-Leu-Cys(SEQ ID NO:34);

Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Asn-Val-Asp-His-Xaa,-Xaa,-Ile-Cys(SEQ ID NO:35);

5 Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ser-Gly-Xaa,-Thr-Gln-Xaa,-Xaa,-Cys-Arg-Xaa,-Ser (SEQ ID NO:36);

Xaa,-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ser-Gly-Asn-Asn-Xaa,-Xaa,-Phe-Cys-Arg-Gln (SEQ ID NO:37);

10 Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ser-Gly-Asn-Asn-Xaa,-Xaa,-Phe-Cys-Arg-Gln (SEQ ID NO:38);

Gly-Cys-Cys-Ser-His-Xaa,-Xaa,-Cys-Ala-Met-Asn-Asn-Xaa,-Asp-Xaa,-Cys (SEQ ID NO:39);

Gly-Cys-Cys-Ser-His-Xaa,-Xaa,-Cys-Phe-Leu-Asn-Asn-Xaa,-Asp-Xaa,-Cys (SEQ ID NO:40);

15 Gly-Cys-Cys-Ser-Asn-Xaa,-Xaa,-Cys-Ile-Ala-Xaa,-Asn-Xaa,-His-Met-Cys-Gly (SEQ ID NO:41);

Gly-Cys-Cys-Ser-Asn-Xaa,-Ala-Cys-Ala-Gly-Asn-Asn-Xaa,-His-Val-Cys-Arg-Gln (SEQ ID NO:43);

Gly-Cys-Cys-Ser-Arg-Xaa,-Ala-Cys-Ile-Ala-Asn-Asn-Xaa,-Asp-Leu-Cys(SEQ ID NO:44);

20 Gly-Cys-Cys-Ser-Asn-Xaa,-Val-Cys-His-Val-Xaa,-His-Xaa,-Xaa,-Leu-Cys-Arg-Arg-Arg (SEQ ID NO:45);

Gly-Gly-Cys-Cys-Ser-Phe-Xaa,-Ala-Cys-Arg-Xaa,-Xaa,-Arg-Xaa,-Xaa,-Met-Cys-Gly(SEQ ID NO:46);

25 Xaa,-Xaa,-Cys-Cys-Ser-Asp-Xaa,-Arg-Cys-Asn-Ser-Ser-His-Xaa,-Xaa,-Leu-Cys-Gly(SEQ ID NO:47);

Xaa,-Gln-Cys-Cys-Ser-Asp-Xaa,-Arg-Cys-Asn-Val-Gly-His-Xaa,-Xaa,-Leu-Cys-Gly(SEQ ID NO:48);

Xaa,-Val-Cys-Cys-Ser-Asp-Xaa,-Arg-Cys-Asn-Val-Gly-His-Xaa,-Xaa,-Ile-Cys-Gly (SEQ ID NO:49);

30 Gly-Cys-Cys-Ser-Arg-Xaa,-Xaa,-Cys-Ile-Ala-Asn-Asn-Xaa,-Asp-Leu-Cys (SEQ ID NO:50);

Xaa₅-Gln-Cys-Cys-Ser-His-Leu-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:51);

Gly-Cys-Cys-Ser-Xaa₄-Phe-Asp-Cys-Arg-Met-Met-Phe-Xaa₅-Xaa₁-Met-Cys-Gly-Xaa₃-Arg (SEQ ID NO:52);

5 Gly-Gly-Cys-Cys-Ser-Phe-Ala-Ala-Cys-Arg-Xaa₂-Xaa₄-Arg-Xaa₅-Xaa₁-Met-Cys-Gly(SEQ ID NO:53);

Gly-Gly-Cys-Cys-Phe-His-Xaa₅-Val-Cys-Xaa₄-Ile-Asn-Leu-Leu-Xaa₁-Met-Cys-Arg-Gln-Arg (SEQ ID NO:54);

10 Ser-Ala-Thr-Cys-Cys-Asn-Xaa₄-Xaa₅-Xaa₁-Cys-Xaa₄-Xaa₁-Thr-Xaa₄-Xaa₅-Xaa₁-Ser-Cys-Leu (SEQ ID NO:55);

Ala-Cys-Cys-Ala-Xaa₄-Xaa₅-Xaa₁-Cys-Phe-Xaa₁-Ala-Xaa₄-Xaa₅-Xaa₁-Arg-Cys-Leu (SEQ ID NO:56);

Asn-Ala-Xaa₁-Cys-Cys-Xaa₄-Xaa₅-Xaa₁-Cys-Xaa₄-Xaa₁-Ala-Xaa₄-Xaa₅-Xaa₁-Ile-Cys-Leu (SEQ ID NO:57);

15 Xaa₁-Cys-Cys-Thr-Asn-Xaa₅-Val-Cys-His-Ala-Xaa₁-His-Gln-Xaa₁-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:170);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Leu-Xaa₁-His-Ser-Asn-Leu-Cys (SEQ ID NO:171);

20 Xaa₁-Cys-Cys-Thr-Asn-Xaa₅-Val-Cys-His-Val-Xaa₁-His-Gln-Xaa₁-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:172);

Xaa₆-Xaa₁-Cys-Cys-Ser-Xaa₄-Xaa₅-Ala-Cys-Asn-Leu-Asp-His-Xaa₅-Xaa₁-Leu-Cys (SEQ ID NO:173);

Xaa₅-Xaa₁-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Asn-Ser-Thr-His-Xaa₅-Xaa₁-Leu-Cys-Gly(SEQ ID NO:174);

25 Leu-Asn-Cys-Cys-Met-Ile-Xaa₅-Xaa₁-Cys-Xaa₃-Xaa₂-Xaa₄-Gly-Asp-Arg-Cys-Ser-Xaa₁-Val-Arg (SEQ ID NO:175);

Ala-Phe-Gly-Cys-Cys-Asp-Leu-Ile-Xaa₅-Cys-Leu-Xaa₁-Arg-Xaa₄-Gly-Asn-Arg-Cys-Asn-Xaa₁-Val-His (SEQ ID NO:176);

30 Leu-Gly-Cys-Cys-Asn-Val-Thr-Xaa₅-Cys-Xaa₃-Xaa₁-Xaa₂-Xaa₄-Gly-Asp-Xaa₂-Cys-Asn-Xaa₁-Val-Arg (SEQ ID NO:177);

Asp-Xaa₁-Cys-Cys-Ser-Asn-Xaa₅-Ala-Cys-Arg-Val-Asn-Asn-Xaa₅-His-Val-Cys-Arg-Arg-Arg (SEQ ID NO:178);

Leu-Asn-Cys-Cys-Ser-Ile-Xaa,-Gly-Cys-Xaa₃-Asn-Xaa₁-Xaa₄-Xaa₂-Asp-Arg-Cys-Ser-Xaa₂-Val-Arg (SEQ ID NO:179);

Gly-Gly-Cys-Cys-Ser-His-Xaa₃-Val-Cys-Xaa₄-Phe-Asn-Asn-Xaa₅-Gln-Met-Cys-Arg (SEQ ID NO:180);

5 Gly-Gly-Cys-Cys-Ser-His-Xaa₃-Val-Cys-Asn-Leu-Asn-Asn-Xaa₅-Gln-Met-Cys-Arg (SEQ ID NO:181);

Gly-Cys-Cys-Ser-His-Xaa₃-Xaa₅-Cys-Xaa₄-Ala-Asn-Asn-Gln-Ala-Xaa₄-Cys-Asn (SEQ ID NO:182);

10 Gly-Gly-Cys-Cys-Ser-His-Xaa₃-Ala-Cys-Ser-Val-Thr-His-Xaa₅-Xaa₁-Leu-Cys (SEQ ID NO:183);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₅-Ala-Cys-Ser-Val-Xaa₁-His-Gln-Asp-Leu-Cys-Asp (SEQ ID NO:184);

Val-Ser-Cys-Cys-Val-Val-Arg-Xaa₅-Cys-Xaa₃-Ile-Arg-Xaa₄-Gln-Xaa₁-Xaa₄-Cys-Leu-Xaa₁-Ala-Asp-Xaa₅-Arg-Thr-Leu (SEQ ID NO:185);

15 Xaa₆-Asn-Cys-Cys-Ser-Ile-Xaa₃-Gly-Cys-Xaa₃-Xaa₁-Xaa₂-Xaa₄-Gly-Asp-Xaa₂-Cys-Ser-Xaa₁-Val-Arg (SEQ ID NO:186);

Gly-Cys-Cys-Ser-Asn-Xaa₃-Val-Cys-His-Leu-Xaa₁-His-Xaa₅-Asn-Ala-Cys (SEQ ID NO:187);

20 Gly-Cys-Cys-Ser-Asn-Xaa₃-Ile-Cys-Xaa₄-Phe-Asn-Asn-Xaa₅-Arg-Ile-Cys-Arg (SEQ ID NO:188);

Xaa₁-Cys-Cys-Ser-Gln-Xaa₅-Xaa₃-Cys-Arg-Xaa₃-Xaa₂-His-Xaa₅-Xaa₁-Leu-Cys-Ser (SEQ ID NO:189);

Gly-Cys-Cys-Ser-His-Xaa₃-Ala-Cys-Ala-Gly-Asn-Asn-Gln-His-Ile-Cys (SEQ ID NO:190);

Gly-Cys-Cys-Ala-Val-Xaa₃-Ser-Cys-Arg-Leu-Arg-Asn-Xaa₅-Asp-Leu-Cys-Gly-Gly (SEQ

25 ID NO:191);

Gly-Cys-Cys-Ser-His-Xaa₃-Ala-Cys-Asn-Val-Asn-Asn-Xaa₅-His-Ile-Cys (SEQ ID NO:192);

Thr-Xaa₃-Xaa₁-Xaa₂-Cys-Cys-Xaa₃-Asn-Xaa₃-Xaa₅-Cys-Phe-Ala-Thr-Asn-Ser-Asp-Ile-Cys-Gly (SEQ ID NO:193);

30 Asp-Ala-Cys-Cys-Ser-Asp-Xaa₃-Arg-Cys-Ser-Gly-Xaa₂-His-Gln-Asp-Leu-Cys (SEQ ID NO:194);

Xaa₁-Asp-Cys-Cys-Ser-Asp-Xaa₃-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Leu-Cys (SEQ ID NO:195);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Ser-Asn-Ala-His-Ile-Cys (SEQ ID NO:196);
Xaa₁-Asp-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys (SEQ ID
NO:197);
Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Asn-Asn-Xaa₅-His-Ile-Cys (SEQ ID NO:198);
5 Gly-Cys-Cys-Gly-Asn-Xaa₅-Ser-Cys-Ser-Ile-His-Ile-Xaa₅-Xaa₄-Val-Cys-Asn (SEQ ID
NO:199);
Thr-Asp-Ser-Xaa₁-Xaa₁-Cys-Cys-Leu-Asp-Ser-Arg-Cys-Ala-Gly-Gln-His-Gln-Asp-Leu-
Cys-Gly (SEQ ID NO:200);
Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₅-Cys-Xaa₄-Ala-Asn-Asn-Gln-Ala-Xaa₄-Cys-Asn (SEQ ID
10 NO:201);
Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Val-Asn-Asn-Xaa₅-Asp-Ile-Cys (SEQ ID NO:202);
Gly-Xaa₂-Cys-Cys-Ile-Asn-Asp-Ala-Cys-Arg-Ser-Xaa₂-His-Xaa₅-Gln-Xaa₄-Cys-Ser (SEQ
ID NO:203);
Gly-Cys-Cys-Xaa₄-Asn-Ile-Ala-Cys-Arg-Ile-Asn-Asn-Xaa₅-Arg-Xaa₄-Cys-Arg (SEQ ID
15 NO:204);
Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Arg-Phe-Asn-Xaa₄-Xaa₅-Xaa₂-Xaa₄-Cys-Gly (SEQ ID
NO:205);
Asp-Xaa₁-Cys-Cys-Ala-Ser-Xaa₅-Xaa₅-Cys-Arg-Leu-Asn-Asn-Xaa₅-Xaa₄-Val-Cys-His
(SEQ ID NO:206);
20 Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-Xaa₃-Gln-Asn-Asn-Ala-Xaa₁-Xaa₄-Cys-Arg-Xaa₁-Ser
(SEQ ID NO:207);
Gly-Cys-Cys-Ser-His-Xaa₅-Xaa₅-Cys-Ala-Gln-Asn-Asn-Gln-Asp-Xaa₄-Cys (SEQ ID
NO:208);
25 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Gly-Asn-Asn-Arg-Xaa₁-Xaa₄-Cys-Arg-Xaa₁-Ser
(SEQ ID NO:209);
Asp-Xaa₁-Cys-Cys-Ser-Xaa₄-Xaa₅-Asp-Cys-Gly-Ala-Asn-His-Xaa₅-Xaa₁-Ile-Cys-Gly (SEQ
ID NO:210);
Xaa₁-Cys-Cys-Ser-Gln-Xaa₅-Xaa₅-Cys-Arg-Xaa₃-Xaa₂-His-Xaa₅-Xaa₁-Leu-Cys-Ser (SEQ
ID NO:211);
30 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Asn-Asn-Xaa₅-His-Ile-Cys (SEQ ID NO:212);
Gly-Cys-Cys-Ser-Asp-Xaa₁-Ser-Cys-Asn-Val-Asn-Asn-Xaa₅-Asp-Xaa₄-Cys (SEQ ID
NO:213);

Xaa₁-Xaa₁-Cys-Cys-Ser-Asp-Xaa₁-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys-Arg (SEQ ID NO:214);

Gly-Gly-Cys-Cys-Ser-Asn-Xaa₁-Ala-Cys-Leu-Val-Asn-His-Leu-Xaa₁-Met-Cys (SEQ ID NO:215);

5 Arg-Asp-Xaa₁-Cys-Cys-Phe-Asn-Xaa₁-Ala-Cys-Asn-Val-Asn-Asn-Xaa₁-Gln-Ile-Cys (SEQ ID NO:216);

Cys-Cys-Ser-Asp-Xaa₁-Ser-Cys-Xaa₁-Arg-Leu-His-Ser-Leu-Ala-Cys-Thr-Gly-Ile-Val-Asn-Arg (SEQ ID NO:217);

Cys-Cys-Thr-Asn-Xaa₁-Ala-Cys-Leu-Val-Asn-Asn-Ile-Arg-Phe-Cys-Gly(SEQIDNO:218);

10 Asp-Xaa₁-Cys-Cys-Ser-Asp-Xaa₁-Arg-Cys-His-Gly-Asn-Asn-Arg-Asp-His-Cys-Ala (SEQ ID NO:219);

Asp-Cys-Cys-Ser-His-Xaa₁-Leu-Cys-Arg-Leu-Phe-Val-Xaa₁-Gly-Leu-Cys-Ile (SEQ ID NO:220);

Gly-Cys-Cys-Ser-His-Xaa₁-Val-Cys-Xaa₂-Val-Arg-Xaa₄-Xaa₅-Asp-Leu-Cys-Arg (SEQ ID 15 NO:221);

Gly-Cys-Cys-Ser-His-Xaa₁-Ala-Cys-Asn-Val-Asn-Asn-Xaa₁-His-Ile-Cys(SEQIDNO:222);

Gly-Cys-Cys-Ser-His-Xaa₁-Val-Cys-Xaa₂-Val-Arg-Xaa₄-Ser-Asp-Met-Cys (SEQ ID NO:223);

Gly-Gly-Cys-Cys-Ser-His-Xaa₁-Ala-Cys-Xaa₂-Val-His-Phe-Xaa₁-His-Ser-Cys (SEQ ID 20 NO:224);

Val-Cys-Cys-Ser-Asn-Xaa₁-Val-Cys-His-Val-Asp-His-Xaa₅-Xaa₁-Leu-Cys-Arg-Arg-Arg-Arg (SEQ ID NO:225);

Gly-Cys-Cys-Ser-His-Xaa₁-Val-Cys-Asn-Leu-Ser-Asn-Xaa₁-Gln-Ile-Cys-Arg (SEQ ID NO:226);

25 Xaa₆-Xaa₁-Cys-Cys-Ser-His-Xaa₁-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:227);

Gly-Cys-Cys-Ser-Asn-Xaa₁-Ala-Cys-Leu-Val-Asn-His-Ile-Arg-Phe-Cys-Gly (SEQ ID NO:228);

Asp-Cys-Cys-Asp-Asp-Xaa₁-Ala-Cys-Thr-Val-Asn-Asn-Xaa₁-Gly-Leu-Cys-Thr (SEQ ID 30 NO:229); and

Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₁-Cys-Ile-Ala-Xaa₂-Asn-Xaa₅-His-Met-Cys-Gly-Gly-Arg-Arg (SEQ ID NO:230),

wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; Xaa₆ is Gln or pyro-Glu; and the C-terminus contains a carboxyl or amide group. The halo is preferably bromine, chlorine or iodine, more preferably iodine for Tyr and bromine for Trp. In addition, the His residues may be substituted with halo-His; the Arg residues may be substituted by Lys, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Tyr residues may be substituted with any unnatural hydroxy containing amino acid; the Ser residues may be substituted with Thr; the Thr residues may be substituted with Ser; and the Phe and Trp residues may be substituted with any unnatural aromatic amino acid. The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

More specifically, the present invention is directed to the following α -conotoxin peptides of general formula III:

- | | |
|--------|---|
| SmI: | SEQ ID NO:22, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| OB-29: | SEQ ID NO:23, wherein Xaa ₁ is Glu, Xaa ₃ is Tyr and Xaa ₅ is Pro; |
| Tx1.1: | SEQ ID NO:24, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| R1.1A: | SEQ ID NO:25, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| R1.1B: | SEQ ID NO:26, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Om-9: | SEQ ID NO:27, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Om-10: | SEQ ID NO:28, wherein Xaa ₅ is Pro; |
| Om-21: | SEQ ID NO:29, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Om-25: | SEQ ID NO:30, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Om-27: | SEQ ID NO:31, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Om-28: | SEQ ID NO:32, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Bt1.2: | SEQ ID NO:33, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Bt1.4: | SEQ ID NO:34, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |
| Da1.1: | SEQ ID NO:35, wherein Xaa ₁ is Glu and Xaa ₅ is Pro; |

- OB-20: SEQ ID NO:36, wherein Xaa₁ is Glu, Xaa₂ is Lys and Xaa₃ is Pro;
- TI: SEQ ID NO:37, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- TIB: SEQ ID NO:38, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Pn1.1: SEQ ID NO:39, wherein Xaa₅ is Pro;
- 5 Pn1.2: SEQ ID NO:40, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- T1: SEQ ID NO:41, wherein Xaa₂ is Lys and Xaa₅ is Pro;
- TIA: SEQ ID NO:43, wherein Xaa₅ is Pro;
- Da1.2: SEQ ID NO:44, wherein Xaa₅ is Pro;
- Cr1.2: SEQ ID NO:45, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- 10 Sl1.2: SEQ ID NO:46, wherein Xaa₁ is Glu, Xaa₂ is Lys and Xaa₅ is Pro;
- Tx1.3: SEQ ID NO:47, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Da1.3: SEQ ID NO:48, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Da1.4: SEQ ID NO:49, wherein Xaa₁ is Glu, Xaa₃ is Pro and Xaa₆ is Gln;
- Tx1.2: SEQ ID NO:50, wherein Xaa₅ is Pro;
- 15 Om-35: SEQ ID NO:51, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Sl1.1: SEQ ID NO:52, wherein Xaa₁ is Glu, Xaa₃ is Trp, Xaa₄ is Tyr and Xaa₅ is Pro;
- Sl1.6: SEQ ID NO:53, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;
- 20 Sl1.7: SEQ ID NO:54, wherein Xaa₁ is Glu Xaa₄ is Tyr and Xaa₅ is Pro;
- Bt1.1: SEQ ID NO:55, wherein Xaa₁ is Glu Xaa₄ is Tyr and Xaa₅ is Pro;
- Bt1.3: SEQ ID NO:56, wherein Xaa₁ is Glu Xaa₄ is Tyr and Xaa₅ is Pro;
- Bt1.5: SEQ ID NO:57, wherein Xaa₁ is Glu Xaa₄ is Tyr and Xaa₅ is Pro;
- A1.4: SEQ ID NO:170, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- 25 A1.5: SEQ ID NO:171, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- A1.6: SEQ ID NO:172, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Af1.1: SEQ ID NO:173, wherein Xaa₁ is Glu Xaa₄ is Tyr, Xaa₃ is Pro and Xaa₆ is Gln;
- Af1.2: SEQ ID NO:174, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- 30 Ar1.2: SEQ ID NO:175, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp, Xaa₄ is Try and Xaa₅ is Pro;
- Ar1.3: SEQ ID NO:176, wherein Xaa₁ is Glu, Xaa₄ is Tyr and Xaa₅ is Pro;

- Ar1.4: SEQ ID NO:177, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp, Xaa₄ is Try and Xaa₅ is Pro;
- Ar1.5: SEQ ID NO:178, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Ar1.6: SEQ ID NO:179, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp, Xaa₄ is Try and Xaa₅ is Pro;
- Ay1.2: SEQ ID NO:180, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
- Ay1.3: SEQ ID NO:181, wherein Xaa₅ is Pro;
- Bn1.4: SEQ ID NO:182, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
- Bt1.8: SEQ ID NO:183, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Bt1.9: SEQ ID NO:184, wherein Xaa₁ is Glu, Xaa₄ is Tyr and Xaa₅ is Pro;
- Ca1.3: SEQ ID NO:185, wherein Xaa₁ is Glu, Xaa₃ is Trp, Xaa₄ is Try and Xaa₅ is Pro;
- Ca1.4: SEQ ID NO:186, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp, Xaa₄ is Try, Xaa₅ is Pro and Xaa₆ is Gln;
- C1.2: SEQ ID NO:187, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- C1.3: SEQ ID NO:188, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
- Ep1.2: SEQ ID NO:189, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp and Xaa₅ is Pro;
- G1.1: SEQ ID NO:190, wherein Xaa₅ is Pro;
- G1.3: SEQ ID NO:191, wherein Xaa₅ is Pro;
- Im1.3: SEQ ID NO:192, wherein Xaa₅ is Pro;
- Lv1.2: SEQ ID NO:193, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Lv1.3: SEQ ID NO:194, wherein Xaa₂ is Lys and Xaa₅ is Pro;
- Lv1.4: SEQ ID NO:195, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Lv1.6: SEQ ID NO:196, wherein Xaa₅ is Pro;
- Lv1.7: SEQ ID NO:197, wherein Xaa₁ is Glu and Xaa₅ is Pro;
- Lv1.8: SEQ ID NO:198, wherein Xaa₅ is Pro;
- Lv1.9: SEQ ID NO:199, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
- Lv1.10: SEQ ID NO:200, wherein Xaa₅ is Glu;
- Mr1.3: SEQ ID NO:201, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
- Mr1.4: SEQ ID NO:202, wherein Xaa₅ is Pro;
- Ms1.1: SEQ ID NO:203, wherein Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;

- Ms1.6: SEQ ID NO:204, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
O1.1: SEQ ID NO:205, wherein Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;
O1.2: SEQ ID NO:206, wherein Xaa₁ is Glu, Xaa₄ is Tyr and Xaa₅ is Pro;
O1.4: SEQ ID NO:207, wherein Xaa₁ is Glu, Xaa₃ is Trp, Xaa₄ is Tyr and Xaa₅ is Pro;
5 O1.7: SEQ ID NO:208, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
O1.8: SEQ ID NO:209, wherein Xaa₁ is Glu, Xaa₄ is Tyr and Xaa₅ is Pro;
Om1.2: SEQ ID NO:210, wherein Xaa₁ is Glu, Xaa₄ is Tyr and Xaa₅ is Pro;
Om1.3: SEQ ID NO:211, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₃ is Trp and Xaa₅ is Pro;
10 Om1.4: SEQ ID NO:212, wherein Xaa₅ is Pro;
Om1.5: SEQ ID NO:213, wherein Xaa₄ is Tyr and Xaa₅ is Pro;
Om1.6: SEQ ID NO:214, wherein Xaa₁ is Glu and Xaa₅ is Pro;
P1.4: SEQ ID NO:215, wherein Xaa₁ is Glu and Xaa₅ is Pro;
15 P1.5: SEQ ID NO:216, wherein Xaa₅ is Pro;
P1.6: SEQ ID NO:217, wherein Xaa₃ is Trp and Xaa₅ is Pro;
P1.8: SEQ ID NO:218, wherein Xaa₅ is Pro;
Rg1.1: SEQ ID NO:219, wherein Xaa₁ is Glu and Xaa₅ is Pro;
Rg1.3: SEQ ID NO:220, wherein Xaa₅ is Pro;
20 Rg1.4: SEQ ID NO:221, wherein Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;
Rg1.5: SEQ ID NO:222, wherein Xaa₅ is Pro;
Rg1.8: SEQ ID NO:223, wherein Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro;
Sm1.4: SEQ ID NO:224, wherein Xaa₂ is Lys and Xaa₅ is Pro;
Sm1.5: SEQ ID NO:225, wherein Xaa₁ is Glu and Xaa₅ is Pro;
25 S1.5: SEQ ID NO:226, wherein Xaa₅ is Pro;
Tx1.5: SEQ ID NO:227, wherein Xaa₁ is Glu, Xaa₅ is Pro and Xaa₆ is Gln;
T1.1: SEQ ID NO:228, wherein Xaa₅ is Pro;
Vr1.3: SEQ ID NO:229, wherein Xaa₅ is Pro; and
Tb: SEQ ID NO:230, wherein Xaa₂ is Lys and Xaa₅ is Pro.
30 The C-terminus preferably contains a carboxyl group for the peptides OB-29, Tx1.1, R1.1A, R1.1B, Om-9, Om-10, Om-21, Om-25, Om-27, Om-28, Cr1.2, Om-35, Bt1.1, Bt1.3, Bt1.5, A1.4, A1.6, Ar1.2, Ar1.3, Ar1.4, Ar1.5, Ar1.6, Ca1.3, Ca1.4, Ep1.2, Lv1.9, O1.2, Om1.3, Om1.6, P1.6, Rg1.1,

Rg1.3, Rg1.4, Sm1.5, Tx1.5 and Vr1.3. The C-terminus of the other peptides preferably contains an amide group.

The present invention is also directed to the novel specific α -conotoxin peptides having the formulas:

5 Cys-Cys-Thr-Ile-Xaa₅-Ser-Cys-Xaa₄-Xaa₁-Xaa₂-Xaa₂-Ile-Xaa₂-Ala-Cys-Val-Phe (SEQ ID NO:231) and

Gly-Cys-Cys-Gly-Asn-Xaa₅-Ala-Cys-Ser-Gly-Ser-Ser-Xaa₂-Asp-Ala-Xaa₅-Ser-Cys (SEQ ID NO:232),

wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group. The halo is preferably bromine, chlorine or iodine, more preferably iodine for Tyr. In addition, the His residues may be substituted with halo-His; the Arg residues may be substituted by Lys, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoarginine, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; the Tyr residues may be substituted with any unnatural hydroxy containing amino acid; the Ser residues may be substituted with Thr; the Thr residues may be substituted with Ser; and the Phe residues may be substituted with any unnatural aromatic amino acid. The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L). The Tyr residues may be substituted with the 3-hydroxyl or 2-hydroxyl isomers and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic bioisoteric amino acid surrogate, e.g., tetrazolyl derivatives of Gly and Ala.

More specifically, the present invention is directed to the following α -conotoxin peptides:

25 G1.2: SEQ ID NO:231, wherein Xaa₁ is Glu, Xaa₂ is Lys, Xaa₄ is Tyr and Xaa₅ is Pro; and

Rg1.12: SEQ ID NO:232, wherein Xaa₂ is Lys and Xaa₅ is Pro.

The C-terminus of G1.2 preferably contains a carboxyl group, and the C-terminus of Rg1.12 preferably contains an amide group.

30 Examples of unnatural aromatic amino acid include, but are not limited to, such as nitro-Phe, 4-substituted-Phe wherein the substituent is C₁-C₃ alkyl, carboxyl, hydroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, -SO₃H and -NHAc. Examples of unnatural hydroxy containing amino

acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of unnatural basic amino acids include, but are not limited to, N-1-(2-pyrazolinyl)-Arg, 2-(4-piperinyl)-Gly, 2-(4-piperinyl)-Ala, 2-[3-(2S)pyrrolininyl]-Gly and 2-[3-(2S)pyrrolininyl]-Ala. These and other unnatural basic amino acids, unnatural hydroxy containing amino acids or unnatural aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also <http://www.amino-acids.com>), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA.

10 Optionally, in the peptides of general formulas I, II and III and the specific peptides described above, the Asn residues may be modified to contain an N-glycan and the Ser and Thr residues may be modified to contain an O-glycan. In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The glycan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

25 Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797, filed 19 October 1999 and in PCT Application No. PCT/US99/24380, filed 19 October 1999, both incorporated herein by reference. A preferred glycan is Gal(β1→3)GalNAc(α1→).

Optionally, in the peptides of general formulas I and II and the specific peptides described above, pairs of Cys residues may be replaced pairwise with Ser/(Glu or Asp) or Lys/(Glu or Asp) combinations. Sequential coupling by known methods (Barnay et al., 2000; Hruby et al., 1994; Bitan et al., 1997) allows replacement of native Cys bridges with lactam bridges.

5 The present invention is further directed to propeptides and nucleic acid sequences encoding the propeptides or peptides as described in further detail herein.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to relatively short peptides (termed α -conotoxins herein), about 10-30 residues in length, which are naturally available in minute amounts in the venom of the cone snails 10 or analogous to the naturally available peptides, and which preferably include two disulfide bonds.

The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of an α -conotoxin peptide. Such a pharmaceutical composition has the capability of acting as antagonists for nicotinic acetylcholine receptors. In one aspect, the α -conotoxins with specificity for neuromuscular junction nicotinic acetylcholine receptors are used 15 as neuromuscular blocking agents for use in conjunction with surgery, as disclosed in U.S. patent application Serial No. 09/_____, filed 21 January 2000 (Attorney Docket No. 2314-178.A) and international patent application No. PCT/US00/_____, filed 21 January 2000 (Attorney Docket No. 2314-138.PCT), each incorporated by reference herein. In a second aspect, additional α -conotoxins 20 and uses for them have been described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,432,155; 5,514,774, each incorporated herein by reference.

In a third aspect additional uses for α -conotoxins are described in U.S. Serial No. 09/219,446, filed 22 December 1998, incorporated herein by reference. In this application, α -conotoxins with specificity for neuronal nicotinic acetylcholine receptors are used for treating disorders regulated at neuronal nicotinic acetylcholine receptors. Such disorders include, but are 25 not limited to, cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders (such as bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder) and small cell lung carcinoma, as well as the localization of small cell lung carcinoma.

The α -conotoxin peptides described herein are sufficiently small to be chemically 30 synthesized. General chemical syntheses for preparing the foregoing α -conotoxin peptides are described hereinafter. Various ones of the α -conotoxin peptides can also be obtained by isolation

and purification from specific *Conus* species using the technique described in U.S. Patent No. 4,447,356 (Olivera et al., 1984), the disclosure of which is incorporated herein by reference.

Although the α -conotoxin peptides of the present invention can be obtained by purification from cone snails, because the amounts of α -conotoxin peptides obtainable from individual snails are very small, the desired substantially pure α -conotoxin peptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For example, the yield from a single cone snail may be about 10 micrograms or less of α -conotoxin peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active α -conotoxin peptides depends of course upon correct determination of the amino acid sequence.

The α -conotoxin peptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). The peptides produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

One method of forming disulfide bonds in the conantokin peptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxypthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology.

Classical solution synthesis is described in detail in the treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S. Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing γ -carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an α -amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the α -amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the α -amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the α -amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected α -amino acid to a suitable resin. Such a starting material can

be prepared by attaching an α -amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or para-methylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae -O-CH₂-resin support, -NH BHA resin support, or -NH-MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the α -amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific α -amino protecting groups may be used as described in Schroder & Lubke (1965).

After removal of the α -amino-protecting group, the remaining α -amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor 5 (1970).

Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH₂Cl₂ (1:1) or in DMF or CH₂Cl₂ alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the α -amino protecting group 10 prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

After the desired amino acid sequence has been completed, the intermediate peptide can be 15 removed from the resin support by treatment with a reagent, such as liquid hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the α -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present 20 in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide 25 while a part of the peptido-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above resins or a benzhydrylamine (BHA) 30 resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-

terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodiimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopro- pylethylamine (DIEA). The Fmoc protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide(DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

Pharmaceutical compositions containing a compound of the present invention or its pharmaceutically acceptable salts as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 10 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of the active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral or parenteral. The compositions may further contain antioxidantizing agents, stabilizing agents, preservatives and the like.

15 For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions. In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by 20 standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See 25 for example, WO 96/11698.

For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, 30 saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending

agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

The active agent is preferably administered in an therapeutically effective amount. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or specialists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Pharmaceutical Sciences*. Typically the conopeptides of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.05 mg/kg to about 100 mg/kg of the active ingredient, more preferably from about 0.1 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved.

Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not otherwise be able to enter the target cells.

The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region. Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

EXAMPLES

The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

5

EXAMPLE 1

Isolation of α -Conotoxins

Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996a). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C₁₈ semi-preparative column (10 x 250 mm) and elution with a linear gradient of acetonitrile in 0.1% TFA. Further purification of bioactive peaks was done on a Vydac C₁₈ analytical column (4.6 x 220 mm) eluted with a gradient of acetonitrile in 0.1% TFA. The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Activity was monitored by assessing block of α 3 β 4 nAChRs expressed in *Xenopus* oocytes.

10

The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

15

In accordance with this method, peptides MII, AuIA, AuIB, AuIC, MAR-1, MAR-2, TI, OB-

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29, EpI, S1.1, Bn1.1, Bn1.2, Ca1.1, Ca1.2, Cn1.1, Cn1.2 and Sm1.3 were obtained.

EXAMPLE 2

Synthesis of Conopeptides

The synthesis of conopeptides, either the mature toxins or the precursor peptides, was separately performed using conventional protection chemistry as described by Cartier et al. (1996).

25

Briefly, the linear chains were built on Rink amide resin by Fmoc procedures with 2-(1H-benzotriol-1-yl)-1,1,3,3,-tetramethyluronium tetrafluoroborated coupling using an ABI model 430A peptide synthesizer with amino acid derivatives purchased from Bachem (Torrence CA). Orthogonal protection was used on cysteines: Cys³ and Cys¹⁶ were protected as the stable Cys(S-acetamidomethyl), while Cys² and Cys⁸ were protected as the acid-labile Cys(S-trityl). After removal of the terminal Fmoc protecting group and cleavage of the peptides from the resins, the

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released peptides were precipitated by filtering the reaction mixture into -10°C methyl t-butyl ether, which removed the protecting groups except on Cys³ and Cys¹⁶. The peptides were dissolved in 0.1% TFA and 60% acetonitrile and purified by RPLC on a Vydac C₁₈ preparative column (22 x 250 mm) and eluted at a flow rate of 20 mL/min with a gradient of acetonitrile in 0.1% TFA.

5 The disulfide bridges in the three conopeptides were formed as described in Cartier et al. (1996). Briefly, the disulfide bridges between Cys² and Cys⁸ were formed by air oxidation which was judged to be complete by analytical RPLC. The monocyclic peptides were purified by RPLC on a Vydac C₁₈ preparative column (22 x 250 mm) and eluted with a gradient of acetonitrile in 0.1% TFA. Removal of S-acetamidomethyl groups and closure of the disulfide bridge between Cys³ and 10 Cys¹⁶ was carried out simultaneously by iodine oxidation. The cyclic peptides were purified by RPLC on a Vydac C₁₈ preparative column (22 x 250 mm) and eluted with a gradient of acetonitrile in 0.1% TFA.

EXAMPLE 3

Isolation of DNA Encoding α -Conotoxins

15 DNA coding for α -conotoxins was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996). Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones 20 having a size of approximately 300 nucleotides were sequenced and screened for similarity in sequence to known α -conotoxins. The DNA sequences and encoded propeptide or peptide sequences are set forth in Tables 1-134.

TABLE 1

DNA Sequence (SEQ ID NO:58) and Protein Sequence (SEQ ID NO:59) of MII

25 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac
Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp

30 aaa gcg tct gac gtg atc acg ctg gcc ctc aag gga tgc tgt tcc aac
Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn

cct gtc tgt cac ttg gag cat tca aac ctt tgt ggt aga aga cgc
Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg

tgatgctcca ggaccctctg aaccacgacg ttgcagca

TABLE 2

DNA Sequence (SEQ ID NO:60) and Protein Sequence (SEQ ID NO:61) of AuIA

5 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc act tca gat cgt gca tct gat ggc agg aag gac gca gcg tct ggc
Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly

 10 ctg atc gct ctg acc atc aag gga tgc tgt tct tat cct ccc tgt ttc
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe

 gcg act aat tca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga
Ala Thr Asn Ser Asp Tyr Cys Gly

 accacgacgt

TABLE 3

15 DNA Sequence (SEQ ID NO:62) and Protein Sequence (SEQ ID NO:63) of AuIB

atg ttc acc gtg ttt ctg ttg gtc gtc ttg gca acc acc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc act tca gat cgt gca tct gat ggc agg aag gac gca gcg tct ggc
Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly

 20 ctg att gct ctg acc atg aag gga tgc tgt tct tat cct ccc tgt ttc
Leu Ile Ala Leu Thr Met Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe

 gcg act aat cca gac tgt ggt cga cga cgc tgatgctcca ggaccctctg
Ala Thr Asn Pro Asp Cys Gly Arg Arg Arg

 aaccacgacgt t

TABLE 4

DNA Sequence (SEQ ID NO:64) and Protein Sequence (SEQ ID NO:65) of Tx1.3

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc tct tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa
Phe Ser Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Lys

 30 gcg tct ggc ctg gtc agt ctg act gac agg aga cca gaa tgc tgt agt
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser

 gat cct cgc tgt aac tcg agt cat cca gaa ctt tgt ggt gga aga cgc
Asp Pro Arg Cys Asn Ser Ser His Pro Glu Leu Cys Gly Gly Arg Arg

 35 tgatgctcca ggaccctctg aaccacgacgt t

TABLE 5

DNA Sequence (SEQ ID NO:66) and Protein Sequence (SEQ ID NO:67) of Tx1.2

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gcc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Val Ser

5 ttc act tca gat cgt gca tct gat gac ggg aaa gcc gct gcg tct gac
Phe Thr Ser Asp Arg Ala Ser Asp Asp Gly Lys Ala Ala Ala Ser Asp

ctg atc act ctg acc atc aag gga tgc tgt tct cgt cct ccc tgt atc
Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile

10 gcg aat aat cca gac ttg tgt ggt tgacgacgct gatgctccag aacggctctga
Ala Asn Asn Pro Asp Leu Cys Gly

accacgacgt tcgagcaatg ttcaccgtgt ttctgttgt tgcgtt

TABLE 6

DNA Sequence (SEQ ID NO:68) and Protein Sequence (SEQ ID NO:69) of Tx1.1

15 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gcc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc act tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa
Phe Thr Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Ala Lys

gcg tct ggc ctg gtc agt ctg act gac agg aga cca caa tgc tgt tct
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser

20 cat cct gcc tgt aac gta gat cat cca gaa att tgt cgt tgaagacgct
His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg

gatgctccag gaccctctga accacgacgt

TABLE 7

DNA Sequence (SEQ ID NO:70) and Protein Sequence (SEQ ID NO:71) of R1.1A

25 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gcc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc act tca ggt cgt cgt aca ttt cat ggc agg aat gcc gca gcc aaa
Phe Thr Ser Gly Arg Arg Thr Phe His Gly Arg Asn Ala Ala Ala Lys

gcg tct ggc ctg gtc agt ctg act gac agg aga cca gaa tgc tgt tct
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser

30 cat cct gcc tgt aac gta gat cat cca gaa att tgt cgt tgaagacgct
His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg

gatgctccag gaccctctga accacgacgt

TABLE 8

DNA Sequence (SEQ ID NO:72) and Protein Sequence (SEQ ID NO:73) of R1.1B

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gcc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

34

ttc act tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa
 Phe Thr Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Ala Lys
 5
 gcg tct ggc ctg gtc agt ctg act gac agg aga cca caa tgc tgt tct
 Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser
 cat cct gcc tgt aac gta gat cat cca gaa att tgc gat tgaagacgct
 His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Asp
 gatgctccag gaccctctga accacgacgt

TABLE 9

DNA Sequence (SEQ ID NO:74) and Protein Sequence (SEQ ID NO:75) of S1.1

10 atg ttc act gtg ttt ctg ttg gtt gtc ttg gca atc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val Val Ser
 ttc cct tta gat cgt gaa tct gat ggc gcg aat gcc gaa gcc cgcc acc
 Phe Pro Leu Asp Arg Glu Ser Asp Gly Ala Asn Ala Glu Ala Arg Thr
 15 cac gat cat gag aag cac gca ctg gac cgcc aat gga tgc tgt agg aat
 His Asp His Glu Lys His Ala Leu Asp Arg Asn Gly Cys Cys Arg Asn
 cct gcc tgt gag agc cac aga tgc ggt tgacgacgct gatgctccag
 Pro Ala Cys Glu Ser His Arg Cys Gly
 gaccctctga accacgacgt tcgagca

TABLE 10

20 DNA Sequence (SEQ ID NO:76) and Protein Sequence (SEQ ID NO:77) of Bn1.1
 atg ttc acc atg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Met Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc gct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aag gac
 Phe Ala Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Lys Asp
 25 aaa gcg tct gac ctg gtc gct ctg acc gtc aag gga tgc tgt tct cat
 Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Ser His
 cct gcc tgt agc gtg aat aat cca gac att tgc ggt tgacgacgct
 Pro Ala Cys Ser Val Asn Asn Pro Asp Ile Cys Gly
 gatgctccag gaccctctga accacgacgt tcgagca

TABLE 11

30 DNA Sequence (SEQ ID NO:78) and Protein Sequence (SEQ ID NO:79) of Bn1.2
 aaa gaa tgc tgt act cat cct gcc tgt cac gtg agt cat cca gaa ctc
 Lys Glu Cys Cys Thr His Pro Ala Cys His Val Ser His Pro Glu Leu
 tgc ggt tgaaaagcga cgtgacgctc caggaccctc tgaaccacga cgttcgagca
 35 Cys Gly

TABLE 12

DNA Sequence (SEQ ID NO:80) and Protein Sequence (SEQ ID NO:81) of Bn1.3

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act gct gtt ctt cca
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro

5 gtc act tta gat cgt gca tct gat gga agg aat gca gca gcc aac gcc
Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala

aaa acg cct cgc ctg atc gcg cca ttc atc agg gat tat tgc tgt cat
Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His

10 aga ggt ccc tgt atg gta tgg tgt ggt tgaagccgct gctgctccag
Arg Gly Pro Cys Met Val Trp Cys Gly

gaccctctga accac

TABLE 13

DNA Sequence (SEQ ID NO:82) and Protein Sequence (SEQ ID NO:83) of Cal1.

15 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc act tca gat cgt gct tct gat ggc agg aat gcc gca gcc aac gcg
Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala

ttt gac ctg atc gct ctg atc gcc agg caa aat tgc tgt agc att ccc
Phe Asp Leu Ile Ala Leu Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro

20 agc tgt tgg gag aaa tat aaa tgt agt taa
Ser Cys Trp Glu Lys Tyr Lys Cys Ser

TABLE 14

DNA Sequence (SEQ ID NO:84) and Protein Sequence (SEQ ID NO:85) of Ca1.2

25 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc act tca gat cgt gcg tct gaa ggc agg aat gct gca gcc aag gac
Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Lys Asp

30 aaa gcg tct gac ctg gtg gct ctg aca gtc agg gga tgc tgt gcc att
Lys Ala Ser Asp Leu Val Ala Leu Thr Val Arg Gly Cys Cys Ala Ile

cgt gaa tgt cgc ttg cag aat gca gcg tat tgt ggt gga ata tac
Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile Tyr

tgtatgctcca ggaccctctg aaccacgacg

TABLE 15

35 DNA Sequence (SEQ ID NO:86) and Protein Sequence (SEQ ID NO:87) of TIB

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

36

ttc cct tca gat att gca act gag ggc agg aat gcc gca gcc aaa gcg
 Phe Pro Ser Asp Ile Ala Thr Glu Gly Arg Asn Ala Ala Lys Ala

 ttt gac ctg ata tct tcg atc gtc aag aaa gga tgc tgt tcc cat cct
 Phe Asp Leu Ile Ser Ser Ile Val Lys Lys Gly Cys Cys Ser His Pro

 5 gcc tgt tcg ggg aat aat cca gaa ttt tgt cgt caa ggt cgcc
 Ala Cys Ser Gly Asn Asn Pro Glu Phe Cys Arg Gln Gly Arg

 tgatgctcca ggaccctctg aaccacgacg t

TABLE 16

DNA Sequence (SEQ ID NO:88) and Protein Sequence (SEQ ID NO:89) of TIA

10 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc cct tca gat ata gca act gag ggc agg aat gcc gca gcc aaa gcg
 Phe Pro Ser Asp Ile Ala Thr Glu Gly Arg Asn Ala Ala Lys Ala

 15 ttt gac ctg ata tct tcg atc gtc agg aaa gga tgc tgt tcc aat ccc
 Phe Asp Leu Ile Ser Ser Ile Val Arg Lys Gly Cys Cys Ser Asn Pro

 gcc tgt gcg ggg aat aat cca cat gtt tgt cgt caa ggt cgcc
 Ala Cys Ala Gly Asn Asn Pro His Val Cys Arg Gln Gly Arg

 tgatgctcca ggaccctctg aaccacgacg t

TABLE 17

20 DNA Sequence (SEQ ID NO:90) and Protein Sequence (SEQ ID NO:91) of SI1.1

 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc
 Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala

 25 aaa gcg tct gac aag atc gct tcg acc ctc aag aga aga gga tgc tgt
 Lys Ala Ser Asp Lys Ile Ala Ser Thr Leu Lys Arg Arg Gly Cys Cys

 tcg tat ttt gac tgt aga atg atg ttt cca gaa atg tgt ggt tgg cga
 Ser Tyr Phe Asp Cys Arg Met Met Phe Pro Glu Met Cys Gly Trp Arg

 30 ggc tgatgctcca ggaccctctg aaccacgacg t
 Gly

TABLE 18

DNA Sequence (SEQ ID NO:92) and Protein Sequence (SEQ ID NO:93) of SI1.2

35 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc
 Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala

 ata gcg tct gac aag atc gct tcg acc ctc agg aga gga gga tgc tgt
 Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys

tct ttt cct gcc tgt aga aag tat cgt cca gaa atg tgt ggt gga cga
 Ser Phe Pro Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg
 cgc tgatgctcca ggaccctctg aaccacgacg t
 Arg

5

TABLE 19

DNA Sequence (SEQ ID NO:94) and Protein Sequence (SEQ ID NO:95) of SI1.3

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Ala Thr Thr Val Val Ser

10

ttc act tca gat cat gaa tct gat cgc ggt gat gcc caa acc atc caa
 Phe Thr Ser Asp His Glu Ser Asp Arg Gly Asp Ala Gln Thr Ile Gln

gaa gtg ttt gag atg ttc gct ctg gac agc gat gga tgc tgt tgg cat
 Glu Val Phe Glu Met Phe Ala Leu Asp Ser Asp Gly Cys Cys Trp His

cct gct tgt ggc aga cac tat tgt ggt cga aga cgc tgatgctcca
 Pro Ala Cys Gly Arg His Tyr Cys Gly Arg Arg Arg

15

ggaccctctg aaccacgacg t

TABLE 20

DNA Sequence (SEQ ID NO:96) and Protein Sequence (SEQ ID NO:97) of SI1.6

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Ala Thr Thr Val Val Ser

20

ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc
 Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala

ata gcg tct gac aag atc gct tcg acc ctc agg aga gga gga tgc tgt
 Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys

25

tct ttt gct gcc tgt aga aag tat cgt cca gaa atg tgt ggt gga cga
 Ser Phe Ala Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg

cgc tgatgct
 Arg

TABLE 21

DNA Sequence (SEQ ID NO:98) and Protein Sequence (SEQ ID NO:99) of SI1.7

30

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Leu Ala Thr Thr Val Val Ser

ttc aat tca gat cgt gca tta ggt ggc agg aat gct gca gcc aaa gcg
 Phe Asn Ser Asp Arg Ala Leu Gly Gly Arg Asn Ala Ala Lys Ala

35

tct gac aag atc ctt tcg aac ctc agg aga gga gga tgc tgt ttt cat
 Ser Asp Lys Ile Leu Ser Asn Leu Arg Arg Gly Gly Cys Cys Phe His

cct gtc tgt tac atc aat ctt cta gaa atg tgt cgt caa cga ggc
 Pro Val Cys Tyr Ile Asn Leu Glu Met Cys Arg Gln Arg Gly

tgatcgatcca ggaccctctg aaccacgacg t

TABLE 22

DNA Sequence (SEQ ID NO:100) and Protein Sequence (SEQ ID NO:101) of Cn1.1

```

atg ttc acc gtg ttt ctg ttg gtc ttg aca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Val Val Ser
5
ttc cct tca gat agt gca tct gat gtc agg gat gac gaa gcc aaa gac
Phe Pro Ser Asp Ser Ala Ser Asp Val Arg Asp Asp Glu Ala Lys Asp
gaa agg tct gac atg tac aaa tcg aaa cgg aat gga cgc tgt tgc cat
Glu Arg Ser Asp Met Tyr Lys Ser Lys Arg Asn Gly Arg Cys Cys His
10
cct gcc tgt ggc aaa cac ttt agt tgt gga cgc tgatgctcca ggaccctctg
Pro Ala Cys Gly Lys His Phe Ser Cys Gly Arg
aaccacgacg t

```

TABLE 23

DNA Sequence (SEQ ID NO:102) and Protein Sequence (SEQ ID NO:103) of SmI

```

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
15
tcc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gag
Ser Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Glu
aaa gcg tct gac gtg atc gcg ctg gcc ctc aag gga tgc tgt tcc aac
Lys Ala Ser Asp Val Ile Ala Leu Ala Leu Lys Gly Cys Cys Ser Asn
20
cct gtc tgt cac ctg gag cat tca aac atg tgt ggt aga aga cgc
Pro Val Cys His Leu Glu His Ser Asn Met Cys Gly Arg Arg Arg
tgatgctcca ggaccctctg aaccacgacg

```

TABLE 24

DNA Sequence (SEQ ID NO:104) and Protein Sequence (SEQ ID NO:105) of Bt1.1

```

atg ttc tcc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
Met Phe Ser Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
25
tcc act tca ggt ggt gca tct ggt ggc agg aag gct gca gcc aaa gcg
Ser Thr Ser Gly Gly Ala Ser Gly Arg Lys Ala Ala Ala Lys Ala
tct aac cgg atc gct ctg acc gtc agg agt gca aca tgc tgt aat tat
Ser Asn Arg Ile Ala Leu Thr Val Arg Ser Ala Thr Cys Cys Asn Tyr
30
cct ccc tgt tac gag act tat cca gaa agt tgt ctg taacgtgaat
Pro Pro Cys Tyr Glu Thr Tyr Pro Glu Ser Cys Leu
catccagagc ttttgtggctg aagacactga tgctccagga ccctctgaac cacgacgt

```

TABLE 25

DNA Sequence (SEQ ID NO:106) and Protein Sequence (SEQ ID NO:107) of Bt1.2

```

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

```

ttc act tca ggt cgt gca ttt cgt ggc agg aat cgc gca gcc gac gac
 Phe Thr Ser Gly Arg Ala Phe Arg Gly Arg Asn Arg Ala Ala Asp Asp
 aaa agg tct gac ctg gcc gct ctg agc gtc agg gga gga tgc tgt tcc
 Lys Arg Ser Asp Ile Ala Ala Leu Ser Val Arg Gly Gly Cys Cys Ser
 5 cat cct gcc tgt gcg gtg aat cat cca gag ctt tgt ggc tgaagacgct
 His Pro Ala Cys Ala Val Asn His Pro Glu Leu Cys Gly
 gatccccagg accctctga accacgacgt

TABLE 26

DNA Sequence (SEQ ID NO:108) and Protein Sequence (SEQ ID NO:109) of Bt1.3

10 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc act tca ggt cgt gca tct ggt ggc agg aat gct gca gcc aaa gcg
 Phe Thr Ser Gly Arg Ala Ser Gly Arg Asn Ala Ala Ala Lys Ala
 15 tct aac cgg atc gct atg gcc atc agc agt gga gca tgc tgt gca tat
 Ser Asn Arg Ile Ala Met Ala Ile Ser Ser Gly Ala Cys Cys Ala Tyr
 cct ccc tgt ttc gag gct tat cca gaa aga tgt ctg taacgtaat
 Pro Pro Cys Phe Glu Ala Tyr Pro Glu Arg Cys Leu
 catccagacc ttttgtggctg aagacgctga tgccccagga ccctctgaac cacgacgt

TABLE 27

20 DNA Sequence (SEQ ID NO:110) and Protein Sequence (SEQ ID NO:111) of Bt1.4
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc act tca gat cgt gca ttt cgt ggc agg aat tcc gca gcc aac gac
 Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ser Ala Ala Asn Asp
 25 aaa agg tct gac ctg gcc gct ctg agc gtc agg aga gga tgc tgc tcc
 Lys Arg Ser Asp Leu Ala Ala Leu Ser Val Arg Arg Gly Cys Cys Ser
 cat ccc gcc tgt agc gtg aat cat cca gag ctt tgt ggt aga aga cgc
 His Pro Ala Cys Ser Val Asn His Pro Glu Leu Cys Gly Arg Arg Arg
 tgatccccca ggaccctctg aaccacgacgt

TABLE 28

DNA Sequence (SEQ ID NO:112) and Protein Sequence (SEQ ID NO:113) of Bt1.5

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc act tca ggt cgt gca tct ggt ggc agg aat gct gca gcc aaa gcg
 Phe Thr Ser Gly Arg Ala Ser Gly Arg Asn Ala Ala Lys Ala
 35 tct aac cgg atc gct ctg atc gtc agg aat gca gaa tgc tgt tat tat
 Ser Asn Arg Ile Ala Leu Ile Val Arg Asn Ala Glu Cys Cys Tyr Tyr

40

cct ccc tgt tac gag gct tat cca gaa att tgt ctg taacgtgaat
 Pro Pro Cys Tyr Glu Ala Tyr Pro Glu Ile Cys Leu
 catccagacc ttttgtggctg aagaccctgaa tgctccagga ccctctgaac cacgacgt

TABLE 29

5 DNA Sequence (SEQ ID NO:114) and Protein Sequence (SEQ ID NO:115) of Pn1.1

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc att tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ile Ser
 ttc act tca gat cgt gca tct gat ggc ggg aat gcc gca gcg tct gac
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Ser Asp
 10 ctg atc gct ctg acc atc aag gga tgc tgt tct cat cct ccc tgt gcc
 Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala
 atg aat aat cca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga
 Met Asn Asn Pro Asp Tyr Cys Gly
 accacgacg

15

TABLE 30

DNA Sequence (SEQ ID NO:116) and Protein Sequence (SEQ ID NO:117) of Pn1.2

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc act tca gat cgt gca tct gat ggc ggg aat gcc gca atg tct gac
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Met Ser Asp
 20 ctg atc gct ctg acc atc aag gga tgc tgt tct cat cct ccc tgt ttc
 Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Phe
 ctg aat aat cca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga
 Leu Asn Asn Pro Asp Tyr Cys Gly
 25 accacgacg

TABLE 31

DNA Sequence (SEQ ID NO:118) and Protein Sequence (SEQ ID NO:119) of Sm1.3

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc cct tca gat cgt gaa tct gat ggc gcg aat gac gaa gcc cgc acc
 Phe Pro Ser Asp Arg Glu Ser Asp Gly Ala Asn Asp Glu Ala Arg Thr
 30 gac gag cct gag gag cac gga ccg gac agg aat gga tgc tgt agg aat
 Asp Glu Pro Glu Glu His Gly Pro Asp Arg Asn Gly Cys Cys Arg Asn
 cct gcc tgt gag agc cac aga tgt ggt tgacgacgct gatgctccag
 Pro Ala Cys Glu Ser His Arg Cys Gly
 35 gaccctctga accacgacg

TABLE 32

DNA Sequence (SEQ ID NO:120) and Protein Sequence (SEQ ID NO:121) of Cr1.2

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 5
 ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc agc gac
 Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ser Asp
 aga gcg tct gac gcg gcc cac cag gga tgc tgt tcc aac cct gtc tgt
 Arg Ala Ser Asp Ala Ala His Gln Gly Cys Cys Ser Asn Pro Val Cys
 10
 cac gtg gaa cat cca gaa ctt tgt cgt aga aga cgc tgatgctcca
 His Val Glu His Pro Glu Leu Cys Arg Arg Arg
 ggaccctctg aaccacgacg

TABLE 33

DNA Sequence (SEQ ID NO:122) and Protein Sequence (SEQ ID NO:123) of Cr1.3

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 15
 ttc cct tca aat cgt gaa tct gat ggc gcg aat gcc gaa gtc cgc acc
 Phe Pro Ser Asn Arg Glu Ser Asp Gly Ala Asn Ala Glu Val Arg Thr
 gac gag cct gag gag cac gac gaa ctg ggc ggg aat gga tgc tgt ggg
 Asp Glu Pro Glu Glu His Asp Glu Leu Gly Gly Asn Gly Cys Cys Gly
 20
 aat cct gac tgt acg agc cac agt tgt gat tgacgacgct gatgctccag
 Asn Pro Asp Cys Thr Ser His Ser Cys Asp
 gaccctctg aaccacgacg

TABLE 34

DNA Sequence (SEQ ID NO:124) and Protein Sequence (SEQ ID NO:125) of Epl

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 25
 ttc act tca gat cgt gca tct gat agc agg aag gac gca gcg tct ggc
 Phe Thr Ser Asp Arg Ala Ser Asp Ser Arg Lys Asp Ala Ala Ser Gly
 ctg atc gct ctg acc atc aag gga tgc tgt tct gat cct cgc tgt aac
 Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser Asp Pro Arg Cys Asn
 30
 atg aat aat cca gac tat tgt ggt tgacgacgct gatgctccag gaccctctg
 Met Asn Asn Pro Asp Tyr Cys Gly
 accacgacg

TABLE 35

DNA Sequence (SEQ ID NO:126) and Protein Sequence (SEQ ID NO:127) of Sn1.1

atg tcc acc gtg ttt ctg ttg gtt gtc ctc gca acc acc gtc gtt tcc
 Met Ser Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

42

ttc act gta gat cgt gca tct gat ggc agg gat gtc gca atc gac gac
 Phe Thr Val Asp Arg Ala Ser Asp Gly Arg Asp Val Ala Ile Asp Asp

 aga ttg gtg tct ctc cct cag atc gcc cat gct gac tgt tgt tcc gat
 Arg Leu Val Ser Leu Pro Gln Ile Ala His Ala Asp Cys Cys Ser Asp

 5 cct gcc tgc aag cag acg ccc ggt tgt cgt taaagacgct gctgctccag
 Pro Ala Cys Lys Gln Thr Pro Gly Cys Arg

 gaccctctga accacgacg

TABLE 36

DNA Sequence (SEQ ID NO:128) and Protein Sequence (SEQ ID NO:129) of Sn1.2

10 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gct tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ala Ser

 ttc att atc gat gat cca tct gat ggc agg aat att gca gtc gac gac
 Phe Ile Ile Asp Asp Pro Ser Asp Gly Arg Asn Ile Ala Val Asp Asp

 15 aga ggg ctt ttc tct acg ctc ttc cat gct gat tgc tgt gaa aat cct
 Arg Gly Leu Phe Ser Thr Leu Phe His Ala Asp Cys Cys Glu Asn Pro

 gcc tgt aga cac acg cag ggt tgt tgatctttgt tcttcaaaga cactgctggc
 Ala Cys Arg His Thr Gln Gly Cys

 ccaggaccct ctgaaccacg acg

TABLE 37

20 DNA Sequence (SEQ ID NO:130) and Protein Sequence (SEQ ID NO:131) of Da1.1

 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc act tca gat cgt gca ttt cgt ggc agg aat gcc gca gcc aaa gag
 Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys Glu

 25 tct ggc ctg gtc ggt ctg acc gac aag acg cga gga tgc tgt tct cat
 Ser Gly Leu Val Gly Leu Thr Asp Lys Thr Arg Gly Cys Cys Ser His

 cct gcc tgt aac gta gat cat cca gaa att tgt ggt tgaagacgct
 Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Gly

 gatgctccag gaccctctga accacgacgt

TABLE 38

DNA Sequence (SEQ ID NO:132) and Protein Sequence (SEQ ID NO:133) of Da1.2

30 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 ttc act tca gat ggt gca tct gat gac agg aaa gcc gct gcg tct gac
 Phe Thr Ser Asp Gly Ala Ser Asp Asp Arg Lys Ala Ala Ser Asp

 35 ctg atc act ctg acc atc aag gga tgc tgt tct cgt cct ccc tgt atc
 Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile

gcg aat aat cca gac ttg tgg ggt cga cga cgc tgatgctcca ggaccctctg
 Ala Asn Asn Pro Asp Leu Cys Gly Arg Arg Arg

TABLE 39

DNA Sequence (SEQ ID NO:134) and Protein Sequence (SEQ ID NO:135) of Da1.3

5 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 tcc act tca ggt cgt cgt gca ttt cat ggc agg aat gcc gca gcc aaa
 Ser Thr Ser Gly Arg Arg Ala Phe His Gly Arg Asn Ala Ala Lys

 10 gcg tct gga ctg gtc ggt ctg act gac agg aga cca caa tgc tgg agt
 Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser

 gat cct cgc tgg aac gta ggt cat cca gaa ctt tgg ggt gga aga cgc
 Asp Pro Arg Cys Asn Val Gly His Pro Glu Leu Cys Gly Arg Arg

 tgatgctcca ggaccctctg aaccacaacg t

TABLE 40

15 DNA Sequence (SEQ ID NO:136) and Protein Sequence (SEQ ID NO:137) of Da1.4

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

 tcc act tca ggt cgt gca ttt cat ggc agg aat gcc gca gcc aaa gcg
 Ser Thr Ser Gly Arg Ala Phe His Gly Arg Asn Ala Ala Lys Ala

 20 tct ggc ctg gtc ggt ctg acc gac aag agg caa gta tgc tgg agt gat
 Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Val Cys Cys Ser Asp

 cct cgc tgg aac gta ggt cat cca gaa att tgg ggt gga aga cgc
 Pro Arg Cys Asn Val Gly His Pro Glu Ile Cys Gly Arg Arg

 tgatgctcca ggaccctctg aaccacgacg t

TABLE 41

DNA Sequence (SEQ ID NO:138) and Protein Sequence (SEQ ID NO:139) of A1.2

atg ttc acc gtg ttt ctg ttg gtt gtc ttg aca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Val Val Ser

 30 ttc cct tca gat agt gca tct ggt ggc agg gat gac gag gcc aaa gac
 Phe Pro Ser Asp Ser Ala Ser Gly Arg Asp Asp Glu Ala Lys Asp

 gaa agg tct gac atg tac gaa ttg aaa cgg aat gga cgc tgg tgc cat
 Glu Arg Ser Asp Met Tyr Glu Leu Lys Arg Asn Gly Arg Cys Cys His

 cct gcc tgg ggt ggc aaa tac gtt aaa tgg gga cgc tgatgctcca
 Pro Ala Cys Gly Gly Lys Tyr Val Lys Cys Gly Arg

 35 ggaccctctc gaaccacg

TABLE 42

DNA Sequence (SEQ ID NO:140) and Protein Sequence (SEQ ID NO:141) of Bu1.1

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

5 ttc tct aca gat gat gaa tct gat ggc tcg aat gaa gaa ccc agc gcc
Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala

gac cag act gcc agg tcc tca atg aac agg gcg cct gga tgc tgt aac
Asp Gln Thr Ala Arg Ser Ser Met Asn Arg Ala Pro Gly Cys Cys Asn

10 aat cct gcc tgt gtg aag cac aga tgt gga tgacgctgat gctccaggac
Asn Pro Ala Cys Val Lys His Arg Cys Gly

cctctgaacc acgacgt

TABLE 43

DNA Sequence (SEQ ID NO:142) and Protein Sequence (SEQ ID NO:143) of Bu1.2

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

15 ttc tct aca gat gat gaa tct gat ggc tcg aat gaa gaa ccc agc gcc
Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala

gac cag gct gcc agg tcc gca atg aac agg ccg cct gga tgc tgt aac
Asp Gln Ala Ala Arg Ser Ala Met Asn Arg Pro Pro Gly Cys Cys Asn

20 aat cct gcc tgt gtg aag cac aga tgt ggt gga tgacgctgat gctccaggac
Asn Pro Ala Cys Val Lys His Arg Cys Gly

cctctgaacc acgacgt

TABLE 44

DNA Sequence (SEQ ID NO:144) and Protein Sequence (SEQ ID NO:145) of Bu1.3

25 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

ttc cct tca gat cgt gac tct gat ggc gcg gat gcc gaa gcc agt gac
Phe Pro Ser Asp Arg Asp Ser Asp Gly Ala Asp Ala Glu Ala Ser Asp

30 gag cct gtt gag ttc gaa agg gac gag aat gga tgc tgt tgg aat cct
Glu Pro Val Glu Phe Glu Arg Asp Glu Asn Gly Cys Cys Trp Asn Pro

tcc tgt ccg agg ccc aga tgt aca gga cga cgc taatgctcca ggaccctctg
Ser Cys Pro Arg Pro Arg Cys Thr Gly Arg Arg

aaccacgacg t

TABLE 45

DNA Sequence (SEQ ID NO:146) and Protein Sequence (SEQ ID NO:170) of Bu1.4

35 atg ttc acc gtg ttt ctg ttg gtc ttg aca acc act gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Val Val Ser

45

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac
 Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp
 aaa gcg tct gac gtg gtc acg ctg gtc ctc aag gga tgc tgt tcc acc
 Lys Ala Ser Asp Val Val Thr Leu Val Leu Lys Gly Cys Ser Thr
 5 cct ccc tgt gct gtg ctg tat tgt ggt aga aga cgc tgatgctcca
 Pro Pro Cys Ala Val Leu Tyr Cys Gly Arg Arg Arg
 ggaccctctg aaccacgacg t

TABLE 46

DNA Sequence (SEQ ID NO:148) and Protein Sequence (SEQ ID NO:149) of Di1.1

10 atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc acc tta
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu
 gat cgt gca tct tat ggc agg tat gcc tca ccc gtc gac aga gca gct tct
 Asp Arg Ala Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser
 15 gcc ctg atc gct cag gcc atc ctt cga gat tgc tgc tcc aat cct cct
 Ala Leu Ile Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro
 tgt gcc cat aat cca gac tgt cgt taaagacgct gcttgctcca
 Cys Ala His Asn Asn Pro Asp Cys Arg
 ggaccctctg aaccacgacg t

TABLE 47

20 DNA Sequence (SEQ ID NO:150) and Protein Sequence (SEQ ID NO:151) of T1
 gga tgc tgt tct aat cct ccc tgt atc gcg aag aat cca cac atg tgt
 Gly Cys Cys Ser Asn Pro Pro Cys Ile Ala Lys Asn Pro His Met Cys
 ggt gga aga cgc tga
 Gly Gly Arg Arg

TABLE 48

DNA Sequence (SEQ ID NO:152) and Protein Sequence (SEQ ID NO:153) of Cn1.2

25 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac
 Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp
 aaa gcg tct gac gtg atc acg ctg gcc ctc aag gga tgc tgt tcc aac
 Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn
 cct gtc tgt cac ttg gag cat tca aac ctt tgt ggt aga aga cgc
 Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg
 35 tgatgctcca ggaccctctg aaccacgacg t

TABLE 49

DNA Sequence (SEQ ID NO:233) and Protein Sequence (SEQ ID NO:234) of Im1.1

tct gat gga aag agt gcc gcg gcc aaa gca aaa ccc tct cac ctg acg
 Ser Asp Gly Lys Ser Ala Ala Ala Lys Ala Lys Pro Ser His Leu Thr
 5 gct cca ttc atc agg gac gaa tgc tgt tcc gat tct cgc tgt ggc aag
 Ala Pro Phe Ile Arg Asp Glu Cys Cys Ser Asp Ser Arg Cys Gly Lys
 aac tgt ctt tga
 Asn Cys Leu

TABLE 50

10 DNA Sequence (SEQ ID NO:235) and Protein Sequence (SEQ ID NO:236) of Im1.2

ttt gat gga agg aat gcc cca gcc gac gac aaa gcg tct gac ctg atc
 Phe Asp Gly Arg Asn Ala Pro Ala Asp Asp Lys Ala Ser Asp Leu Ile
 gct caa atc gtc agg aga gca tgc tgt tcc gat cgt cgc tgt aga tgg
 Ala Gln Ile Val Arg Arg Ala Cys Cys Ser Asp Arg Arg Cys Arg Trp
 15 agg tgt ggt tga
 Arg Cys Gly

TABLE 51

DNA Sequence (SEQ ID NO:237) and Protein Sequence (SEQ ID NO:238) of Rg1.2

20 tct gat gga agg aat gcc gca gcc gac gcc aga gcg tct ccc cgg atc
 Ser Asp Gly Arg Asn Ala Ala Ala Asp Ala Arg Ala Ser Pro Arg Ile
 gct ctt ttc ctc agg ttc aca tgc tgt agg aga ggt acc tgt tcc cag
 Ala Leu Phe Leu Arg Phe Thr Cys Cys Arg Arg Gly Thr Cys Ser Gln
 cac tgt ggt tgaagacact gctgctccag gaccctctga accacgacgt
 His Cys Gly

25

TABLE 52

DNA Sequence (SEQ ID NO:239) and Protein Sequence (SEQ ID NO:240) of Rg1.6

30 tct aat gga agg aat gcc gca gcc gac gcc aaa gcg tct cca cgg atc
 Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile
 gct cca ttc ctc agg gac tat tgc tgt agg aga cat gcc tgt acg ttg
 Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg His Ala Cys Thr Leu
 att tgt ggt tgaagacgct gctgctccag gaccctctga accacgacgt
 Ile Cys Gly

TABLE 53

DNA Sequence (SEQ ID NO:241) and Protein Sequence (SEQ ID NO:242) of Rg1.6A

35 tct aat gga agg aat gcc gca gcc gac gcc aaa gcg tct cca cgg atc

47

Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile
 gct cca ttc ctc agg gac tat tgc tgt agg aga cct ccc tgt acg ttg
 Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg Pro Pro Cys Thr Leu
 att tgt ggt tgaagacgct gctgctccag gaccctctga accacgacgt
 5 Ile Cys Gly

TABLE 54

DNA Sequence (SEQ ID NO:243) and Protein Sequence (SEQ ID NO:244) of Rg1.7

tct aat aaa agg aag aat gcc gca atg ctt gac atg atc gct caa cac
 Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
 10 gcc ata agg ggt tgc tgt tcc gat cct cgc tgt aga tat aga tgt cgt
 Ala Ile Arg Gly Cys Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
 tgaagacgct gctgctccag gaccctctga accacgacgt

TABLE 55

DNA Sequence (SEQ ID NO:245) and Protein Sequence (SEQ ID NO:246) of Rg1.9

15 ttt aat gga agg agt gcc gca gcc gac caa aat gcg cct ggc ctg atc
 Phe Asn Gly Arg Ser Ala Ala Asp Gln Asn Ala Pro Gly Leu Ile
 gct caa gtc gtc aga gga ggg tgc tgt tcc gat ccc cgc tgc gcc tgg
 Ala Gln Val Val Arg Gly Cys Ser Asp Pro Arg Cys Ala Trp
 20 aga tgt ggt tgaagacggtt gctgctccag gaccctctga accacgacgt
 Arg Cys Gly

TABLE 56

DNA Sequence (SEQ ID NO:247) and Protein Sequence (SEQ ID NO:248) of Rg1.10

25 ttt gat gga agg aat gcc gca gcc gac gcc aaa gtg att aac acg gtc
 Phe Asp Gly Arg Asn Ala Ala Asp Ala Lys Val Ile Asn Thr Val
 gct cga atc gcc tgg gat ata tgc tgt tcc gaa cct gac tgt aac cat
 Ala Arg Ile Ala Trp Asp Ile Cys Cys Ser Glu Pro Asp Cys Asn His
 aaa tgt gtt tgaagacgct tctgctccag gaccctctga accacgacgt
 Lys Cys Val

TABLE 57

30 DNA Sequence (SEQ ID NO:249) and Protein Sequence (SEQ ID NO:250) of Rg1.11

tct aat aaa agg aag aat gcc gca atg ctt gac atg atc gct caa cac
 Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
 gcc ata agg ggt tgc tgt tcc gat cct cgc tgt aaa cat cag tgt ggt
 Ala Ile Arg Gly Cys Ser Asp Pro Arg Cys Lys His Gln Cys Gly
 35 tgaagacgct gctgctccag gaccctctga accacgacgt

TABLE 58

DNA Sequence (SEQ ID NO:251) and Protein Sequence (SEQ ID NO:252) of Ms1.7

atc aag aat aca gca gcc agc aac aaa gcg tct agc ctg gtg gct ctt
 Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Ser Ser Leu Val Ala Leu
 5 gtt gtc agg gga tgc tgt tac aat cct gtc tgc aag aaa tat tat tgt
 Val Val Arg Gly Cys Cys Tyr Asn Pro Val Cys Lys Lys Tyr Tyr Cys
 tgg aaa ggc tgatgctcca ggaccctctg aaccacgacg t
 Trp Lys Gly

TABLE 59

10 DNA Sequence (SEQ ID NO:253) and Protein Sequence (SEQ ID NO:254) of P1.7

tct gaa ggc agg aat gct gaa gcc atc gac aac gcc tta gac cag agg
 Ser Glu Gly Arg Asn Ala Glu Ala Ile Asp Asn Ala Leu Asp Gln Arg
 gat cca aag cga cag gag ccg ggg tgc tgt agg cat cct gcc tgt ggg
 Asp Pro Lys Arg Gln Glu Pro Gly Cys Cys Arg His Pro Ala Cys Gly
 15 aag aac aga tgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t
 Lys Asn Arg Cys Gly Arg Arg

TABLE 60

DNA Sequence (SEQ ID NO:255) and Protein Sequence (SEQ ID NO:256) of Ms1.2

20 tct gat ggc agg aat att gca gtc gac gac aga tgg tct ttc tat acg
 Ser Asp Gly Arg Asn Ile Ala Val Asp Asp Arg Trp Ser Phe Tyr Thr
 ctc ttc cat gct act tgc tgt gcc gat cct gac tgt aga ttc cgg ccc
 Leu Phe His Ala Thr Cys Cys Ala Asp Pro Asp Cys Arg Phe Arg Pro
 ggt tgt tgatcttgt tcttcaaaga cgctgctggc ccaggaccct ctgaaccacg
 Gly Cys
 25 acgt

TABLE 61

DNA Sequence (SEQ ID NO:257) and Protein Sequence (SEQ ID NO:258) of Ms1.3

atc aag aat act gca gcc agc aac aaa gcg cct agc ctg gtg gct att
 Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Pro Ser Leu Val Ala Ile
 30 gcc gtc agg gga tgc tgt tac aat cct tcc tgt tgg ccg aaa aca tat
 Ala Val Arg Gly Cys Cys Tyr Asn Pro Ser Cys Trp Pro Lys Thr Tyr
 tgt agt tggaaaaggct gatgctccag gaccctctga accacgacgt
 Cys Ser

TABLE 62

DNA Sequence (SEQ ID NO:259) and Protein Sequence (SEQ ID NO:260) of Ms1.4

tct gat agc agg aat gtc gca atc gag gac aga gtg tct gac ctg cac
 Ser Asp Ser Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu His

5 tct atg ttc ttc gat gtt tct tgc tgt agc aat cct acc tgt aaa gaa
 Ser Met Phe Phe Asp Val Ser Cys Cys Ser Asn Pro Thr Cys Lys Glu

acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc
 Thr Tyr Gly Cys

TABLE 63

10 DNA Sequence (SEQ ID NO:261) and Protein Sequence (SEQ ID NO:262) of Ms1.5

tct gtt ggc agg aat att gca gtc gac gac aga ggg att ttc tct acg
 Ser Val Gly Arg Asn Ile Ala Val Asp Asp Arg Gly Ile Phe Ser Thr

ctc ttc cat gct cat tgc tgt gcc aat ccc atc tgt aaa aac acg ccc
 Leu Phe His Ala His Cys Ala Asn Pro Ile Cys Lys Asn Thr Pro

15 ggt tgt tgatctttgt tcttcaaaga cgctgctggc ccaggaccct ctgaaccacg
 Gly Cys

acgt

TABLE 64

DNA Sequence (SEQ ID NO:263) and Protein Sequence (SEQ ID NO:264) of Ms1.8

20 tcc gat ggc agg aat gtc gca atc gac gac aga gtg tct gac ctg cac
 Ser Asp Gly Arg Asn Val Ala Ile Asp Asp Arg Val Ser Asp Leu His

tct atg ttc ttc gat att gct tgc tgt aac aat cct acc tgt aaa gaa
 Ser Met Phe Phe Asp Ile Ala Cys Cys Asn Pro Thr Cys Lys Glu

25 acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc
 Thr Tyr Gly Cys

tgaaccacga cgt

TABLE 65

DNA Sequence (SEQ ID NO:265) and Protein Sequence (SEQ ID NO:266) of Ms1.9

30 tct gat ggc agg aat gtc gca atc gag gac gac aga gtg tct gac ctg ctc
 Ser Asp Gly Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu Leu

tct atg ctc ttc gat gtt gct tgc tgt agc aat cct gtc tgt aaa gaa
 Ser Met Leu Phe Asp Val Ala Cys Cys Ser Asn Pro Val Cys Lys Glu

acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc
 Thr Tyr Gly Cys

35 tgaaccacga cgt

50

TABLE 66

DNA Sequence (SEQ ID NO:267) and Protein Sequence (SEQ ID NO:268) of Bt1.7

tat gat ggc agg aat gct gcc gcc gac gac aaa gct ttt gac ctg ctg
 Tyr Asp Gly Arg Asn Ala Ala Asp Asp Lys Ala Phe Asp Leu Leu
 5
 gct atg acc ata agg gga gga tgc tgt tcc tat cct ccc tgt atc gcg
 Ala Met Thr Ile Arg Gly Gly Cys Cys Ser Tyr Pro Pro Cys Ile Ala
 agt aat cct aaa tgt ggt gga aga cgc tgatgctcca ggaccctctg
 Ser Asn Pro Lys Cys Gly Arg Arg
 aaccacaacg t

10

TABLE 67

DNA Sequence (SEQ ID NO:269) and Protein Sequence (SEQ ID NO:270) of Lv1.5

ttt gat ggc agg aat gct gca ggc aac gcc aaa atg tcc gcc ctg atg
 Phe Asp Gly Arg Asn Ala Ala Gly Asn Ala Lys Met Ser Ala Leu Met
 15
 gcc ctg acc atc agg gga tgc tgt tcc cat cct gtc tgt agc gcg atg
 Ala Leu Thr Ile Arg Gly Cys Cys Ser His Pro Val Cys Ser Ala Met
 agt cca atc tgt ggc tgaagacgct gatgccccag gaccctctga accacgacgt
 Ser Pro Ile Cys Gly

TABLE 68

DNA Sequence (SEQ ID NO:271) and Protein Sequence (SEQ ID NO:272) of Ms1.10

20
 atc aag aat gct gca gct gac gac aaa gca tct gac ctg ctc tct cag
 Ile Lys Asn Ala Ala Asp Asp Lys Ala Ser Asp Leu Leu Ser Gln
 atc gtc agg aat gct gca tcc aat gac aaa ggg tct gac ctg atg act
 Ile Val Arg Asn Ala Ser Asn Asp Lys Gly Ser Asp Leu Met Thr
 25
 ctt gcc ctc agg gga tgc tgt aaa aat cct tac tgt ggt gcg tcg aaa
 Leu Ala Leu Arg Gly Cys Cys Lys Asn Pro Tyr Cys Gly Ala Ser Lys
 aca tat tgt ggt aga aga cgc tgatgctcca ggaccctctg aaccacgacg t
 Thr Tyr Cys Gly Arg Arg

TABLE 69

DNA Sequence (SEQ ID NO:273) and Protein Sequence (SEQ ID NO:274) of Om1.1

30
 tctgatggca ggaatgcccgc agcgtctgac ctgatggat ctg acc atc aag gga
 Leu Thr Ile Lys Gly
 tgc tgt tct tat ccc tgt ttc gcg act aat cca gac tgt ggt cga
 Cys Cys Ser Tyr Pro Pro Cys Phe Ala Thr Asn Pro Asp Cys Gly Arg
 35
 cga cgc tgatgctcca ggaccctctg aaccacgacg t
 Arg Arg

TABLE 70

DNA Sequence (SEQ ID NO:275) and Protein Sequence (SEQ ID NO:276) of R1.6

ttt gat ggc agg aat gcc gca gcc gac tac aaa ggg tct gaa ttg ctc
 Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr Lys Gly Ser Glu Leu Leu
 5
 gct atg acc gtc agg gga gga tgc tgt tcc tat cct ccc tgt atc gca
 Ala Met Thr Val Arg Gly Gly Cys Ser Tyr Pro Pro Cys Ile Ala
 aat aat cct ctt tgt gct gga aga cgc tga
 Asn Asn Pro Leu Cys Ala Gly Arg Arg

TABLE 71

10 DNA Sequence (SEQ ID NO:277) and Protein Sequence (SEQ ID NO:278) of R1.7

ttt gat ggc agg aat gcc gca gcc gac tac aaa ggg tct gaa ttg ctc
 Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr Lys Gly Ser Glu Leu Leu
 gct atg acc gtc agg gga gga tgc tgt tcc tat cct ccc tgt atc gca
 Ala Met Thr Val Arg Gly Gly Cys Ser Tyr Pro Pro Cys Ile Ala
 15 aat aat cct ttt tgt gct gga aga cgc tga
 Asn Asn Pro Phe Cys Ala Gly Arg Arg

TABLE 72

DNA Sequence (SEQ ID NO:279) and Protein Sequence (SEQ ID NO:280) of Vr1.1

20 tct tat gac agg tat gcc tcg ccc gtc gac aga gcg tct gcc ctg atc
 Ser Tyr Asp Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
 gct cag gcc atc ctt cga gat tgc tgt tcc aat cct ccc tgt tcc caa
 Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ser Gln
 aat aat cca gac tgt atg taaagacgct gcttgctcca ggaccctctg
 Asn Asn Pro Asp Cys Met
 25 aaccacgacg t

TABLE 73

DNA Sequence (SEQ ID NO:281) and Protein Sequence (SEQ ID NO:282) of Vr1.2

tct tat ggc agg tat gcc tca ccc gtc gac aga gcg tct gcc ctg atc
 Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
 30 gct cag gcc atc ctt cga gat tgc tgc tcc aat cct cct tgt gcc cat
 Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ala His
 aat aat cca gac tgt cgt taaagacgct gcttgctcca ggaccctctg
 Asn Asn Pro Asp Cys Arg
 aaccacgacg t

52

TABLE 74

DNA Sequence (SEQ ID NO:283) and Protein Sequence (SEQ ID NO:284) of A1.4

tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct ggc atg agc
 Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Gly Met Ser
 5
 gcg ctg gcc gtc aat gaa tgc tgt acc aac cct gtc tgt cac gcg gaa
 Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Ala Glu
 cat caa gaa ctt tgt gct aga aga cgc tga
 His Gln Glu Leu Cys Ala Arg Arg Arg

TABLE 75

10 DNA Sequence (SEQ ID NO:285) and Protein Sequence (SEQ ID NO:286) of A1.5

tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct gac gtg atc
 Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Ala Ser Asp Val Ile
 acg ctg gcc ctc aag gga tgc tgt tcc aac cct gtc tgt cac ttg gag
 Thr Leu Ala Leu Lys Gly Cys Ser Asn Pro Val Cys His Leu Glu
 15
 cat tca aac ctt tgt ggt aga aga cgc tga
 His Ser Asn Leu Cys Gly Arg Arg Arg

TABLE 76

DNA Sequence (SEQ ID NO:287) and Protein Sequence (SEQ ID NO:288) of A1.6

tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct ggc atg agc
 Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Ala Ser Gly Met Ser
 gcg ctg gcc gtc aat gaa tgc tgt acc aac cct gtc tgt cac gtg gaa
 Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Val Glu
 cat caa gaa ctt tgt gct aga aga cgc tga
 His Gln Glu Leu Cys Ala Arg Arg Arg

25

TABLE 77

DNA Sequence (SEQ ID NO:289) and Protein Sequence (SEQ ID NO:290) of Af1.1

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 30
 ttc act tca gat cgt gca ttt cgt ggc agg aat gcc gca gcc aaa gcg
 Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys Ala
 tct ggc ctg gtc ggt ctg acc gac aag agg caa gaa tgc tgt tct tat
 Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Glu Cys Cys Ser Tyr
 cct gcc tgt aac cta gat cat cca gaa ctt tgt ggt tgaagacgct
 Pro Ala Cys Asn Leu Asp His Pro Glu Leu Cys Gly
 35
 gatgctccag gaccctctga accacgacgt

TABLE 78

DNA Sequence (SEQ ID NO:291) and Protein Sequence (SEQ ID NO:292) of Af1.2

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

5 tcc act tca ggt cgt cgt gca ttt cgt ggc agg aat gcc gca gcc aaa
 Ser Thr Ser Gly Arg Arg Ala Phe Arg Gly Arg Asn Ala Ala Ala Lys

gcg tct gga ctg gtc ggt ctg act gac agg aga cca gaa tgc tgt agt
 Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser

10 gat cct cgc tgt aac tcg act cat cca gaa ctt tgt ggt gga aga cgc
 Asp Pro Arg Cys Asn Ser Thr His Pro Glu Leu Cys Gly Gly Arg Arg

tgatgctcca ggaccctctg aaccacgacg t

TABLE 79

DNA Sequence (SEQ ID NO:293) and Protein Sequence (SEQ ID NO:294) of Ar1.2

15 tct gat ggc agg aat gcc gca gcc aac gcg ttt gac ctg atc gat ctg
 Ser Asp Gly Arg Asn Ala Ala Asn Ala Phe Asp Leu Ile Asp Leu

acc gcc agg cta aat tgc tgt atg att ccc ccc tgt tgg aag aaa tat
 Thr Ala Arg Leu Asn Cys Cys Met Ile Pro Pro Cys Trp Lys Lys Tyr

gga gac aga tgt agt gaa gta cgc tgatgctcca ggaccctctg aaccacgacg
 Gly Asp Arg Cys Ser Glu Val Arg

20 t

TABLE 80

DNA Sequence (SEQ ID NO:295) and Protein Sequence (SEQ ID NO:296) of Ar1.3

tct gat ggc agg aat gcc gca cgc aaa gcg ttt ggc tgc tgc gac tta
 Ser Asp Gly Arg Asn Ala Ala Arg Lys Ala Phe Gly Cys Cys Asp Leu

25 ata ccc tgt ttg gag aga tat ggt aac aga tgt aat gaa gtg cac
 Ile Pro Cys Leu Glu Arg Tyr Gly Asn Arg Cys Asn Glu Val His

tgatgctcca ggaccctctg aaccacgacg cgt

TABLE 81

DNA Sequence (SEQ ID NO:297) and Protein Sequence (SEQ ID NO:298) of Ar1.4

30 tct gat ggc agc aat gcc gca gcc aac gag ttt gac ctg atc gct ctg
 Ser Asp Gly Ser Asn Ala Ala Asn Glu Phe Asp Leu Ile Ala Leu

acc gcc agg cta ggt tgc tgt aac gtt aca ccc tgt tgg gag aaa tat
 Thr Ala Arg Leu Gly Cys Cys Asn Val Thr Pro Cys Trp Glu Lys Tyr

35 gga gac aaa tgt aat gaa gta cgc tgatgcttca ggaccctctg aaccacgacg
 Gly Asp Lys Cys Asn Glu Val Arg

t

TABLE 82

DNA Sequence (SEQ ID NO:299) and Protein Sequence (SEQ ID NO:300) of Ar1.5

tct gat ggc agg aat gtc gca gca aaa gcg ttt cac cgg atc ggc cg
Ser Asp Gly Arg Asn Val Ala Ala Lys Ala Phe His Arg Ile Gly Arg
5 acc atc agg gat gaa tgc tgt tcc aat cct gcc tgt agg gtg aat aat
Thr Ile Arg Asp Glu Cys Cys Ser Asn Pro Ala Cys Arg Val Asn Asn
cca cac gtt tgt aga cga cgc tgatgctcca ggaccctctg aaccacgacg t
Pro His Val Cys Arg Arg Arg

TABLE 83

10 DNA Sequence (SEQ ID NO:301) and Protein Sequence (SEQ ID NO:302) of Ar1.6

tct gat ggc agg aat gcc gca gca aac gcg ttt gac ctg atg cct ctg
Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Phe Asp Leu Met Pro Leu
acc gcc agg cta aat tgc tgt agc att ccc ggc tgt tgg aac gaa tat
Thr Ala Arg Leu Asn Cys Cys Ser Ile Pro Gly Cys Trp Asn Glu Tyr
15 aaa gac aga tgt agt aaa gta cgc tgatgctcca ggaccctctg aaccacgacg
Lys Asp Arg Cys Ser Lys Val Arg
t

TABLE 84

DNA Sequence (SEQ ID NO:303) and Protein Sequence (SEQ ID NO:304) of Ay1.2

20 tctgatggca ggaatgccgc agccgacgac aaagcgtctg acctggtcgc t ctg gtc
Leu Val
gtc agg gga gga tgc tgt tcc cac cct gtc tgt tac ttt aat aat cca
Val Arg Gly Gly Cys Ser His Pro Val Cys Tyr Phe Asn Asn Pro
caa atg tgt cgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t
25 Gln Met Cys Arg Gly Arg Arg

TABLE 85

DNA Sequence (SEQ ID NO:305) and Protein Sequence (SEQ ID NO:306) of Ay1.3

tctgatggca ggaatgccgc agccgacgac aaagcgtctg acctggtcgc t ctg gcc
Leu Ala
30 gtc agg gga gga tgc tgt tcc cac cct gtc tgt aac ttg aat aat cca
Val Arg Gly Gly Cys Ser His Pro Val Cys Asn Leu Asn Asn Pro
caa atg tgt cgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t
Gln Met Cys Arg Gly Arg Arg

TABLE 86

35 DNA Sequence (SEQ ID NO:307) and Protein Sequence (SEQ ID NO:308) of Bt1.8

55

ttt cgt ggc agg aat ccc gca gcc aac gac aaa agg tct gac ctg gcc
 Phe Arg Gly Arg Asn Pro Ala Ala Asn Asp Lys Arg Ser Asp Leu Ala
 gct ctg agc gtc agg gga gga tgc tgt tcc cat cct gcc tgt agc gtg
 Ala Leu Ser Val Arg Gly Gly Cys Cys Ser His Pro Ala Cys Ser Val
 5 act cat cca gag ctt tgt ggc tgaagacgct gatgccccag gaccctctga
 Thr His Pro Glu Leu Cys Gly
 accacgacgt

TABLE 87

DNA Sequence (SEQ ID NO:309) and Protein Sequence (SEQ ID NO:310) of Bt1.9

10 tct gat ggc ggg aat gcc gca gcc aaa gcg tct gac ctg atc gct cag
 Ser Asp Gly Gly Asn Ala Ala Ala Lys Ala Ser Asp Leu Ile Ala Gln
 acc atc agg gga gga tgc tgt tcc tat cct gcc tgt agc gtg gaa cat
 Thr Ile Arg Gly Cys Cys Ser Tyr Pro Ala Cys Ser Val Glu His
 15 caa gac ctt tgt gat gga aga cgc tgatgctcca ggaccctctg aaccacgacg
 Gln Asp Leu Cys Asp Gly Arg Arg
 t

TABLE 88

DNA Sequence (SEQ ID NO:311) and Protein Sequence (SEQ ID NO:312) of Ca1.3

20 tct tat ggc agg aat gcc gca gcc aaa gcg ttt gaa gtg agt tgc tgt
 Ser Tyr Gly Arg Asn Ala Ala Ala Lys Ala Phe Glu Val Ser Cys Cys
 gtc gtt cgc ccc tgt tgg att cgc tat caa gag gaa tgt ctt gaa gca
 Val Val Arg Pro Cys Trp Ile Arg Tyr Gln Glu Glu Cys Leu Glu Ala
 gat ccc agg acc ctc tga
 Asp Pro Arg Thr Leu

TABLE 89

DNA Sequence (SEQ ID NO:313) and Protein Sequence (SEQ ID NO:314) of Ca1.4

tct gat ggc agg aat gcc gca gcc aac gcc ctt gac ctg atc act ctg
 Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Leu Asp Leu Ile Thr Leu
 30 atc gcc agg caa aat tgc tgt agc att ccc ggc tgt tgg gag aaa tat
 Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro Gly Cys Trp Glu Lys Tyr
 gga gac aaa tgt agt gaa gta cgc tga
 Gly Asp Lys Cys Ser Glu Val Arg

TABLE 90

DNA Sequence (SEQ ID NO:315) and Protein Sequence (SEQ ID NO:316) of C1.2

35 tct gat ggc agg aat gaa gca gcc aac gac gaa gcg tct gac gtg atc
 Ser Asp Gly Arg Asn Glu Ala Ala Asn Asp Glu Ala Ser Asp Val Ile

56

gag ctg gcc ctc aag gga tgc tgt tcc aac cct gtc tgt cac ttg gag
 Glu Leu Ala Leu Lys Gly Cys Cys Ser Asn Pro Val Cys His Leu Glu
 cat cca aac gct tgt ggt aga aga cgc tgatgctcca ggaccctctg
 His Pro Asn Ala Cys Gly Arg Arg Arg
 5 aaccacgacg t

TABLE 91

DNA Sequence (SEQ ID NO:317) and Protein Sequence (SEQ ID NO:318) of C1.3

tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct gac ctg gtc
 Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Ala Ser Asp Leu Val
 10 gct ctg gcc gtc agg gga tgc tgt tcc aac cct atc tgt tac ttt aat
 Ala Leu Ala Val Arg Gly Cys Cys Ser Asn Pro Ile Cys Tyr Phe Asn
 aat cca cga att tgt cgt gga aga cgc tgatgctcca ggaccctctg
 Asn Pro Arg Ile Cys Arg Gly Arg Arg
 aaccacgacg t

15

TABLE 92

DNA Sequence (SEQ ID NO:319) and Protein Sequence (SEQ ID NO:320) of Ep1.2

tct cat ggc agg aat gcc gca cgc aaa gcg tct gac ctg atc gct ctg
 Ser His Gly Arg Asn Ala Ala Arg Lys Ala Ser Asp Leu Ile Ala Leu
 20 acc gtc agg gaa tgc tgt tct cag cct ccc tgt cgc tgg aaa cat cca
 Thr Val Arg Glu Cys Cys Ser Gln Pro Pro Cys Arg Trp Lys His Pro
 gaa ctt tgt agt tga
 Glu Leu Cys Ser

TABLE 93

DNA Sequence (SEQ ID NO:321) and Protein Sequence (SEQ ID NO:322) of G1.1

25

tct gat ggc agg aat gac gca gcc aaa gcg ttt gac ctg ata tct tcg
 Ser Asp Gly Arg Asn Asp Ala Ala Lys Ala Phe Asp Leu Ile Ser Ser
 acc gtc aag aaa gga tgc tgt tcc cat cct gcc tgt gcg ggg aat aat
 Thr Val Lys Lys Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn Asn
 30 caa cat att tgt ggc cga aga cgc tgatgctcca ggaccctctg aaccacgacg
 Gln His Ile Cys Gly Arg Arg Arg
 t

TABLE 94

DNA Sequence (SEQ ID NO:323) and Protein Sequence (SEQ ID NO:324) of G1.3

35

tct gat ggc agg aat gcc gca gcc aac gac caa gcg tct gac ctg atg
 Ser Asp Gly Arg Asn Ala Ala Asn Asp Gln Ala Ser Asp Leu Met

57

gct gcg acc gtc agg gga tgc tgt gcc gtt cct tcc tgt cgc ctc cgt
 Ala Ala Thr Val Arg Gly Cys Cys Ala Val Pro Ser Cys Arg Leu Arg
 aat cca gac ctt tgt ggt gga gga cgc tgatgctcca ggaccctctg
 Asn Pro Asp Leu Cys Gly Gly Arg
 5 aaccacgacg t

TABLE 95

DNA Sequence (SEQ ID NO:325) and Protein Sequence (SEQ ID NO:326) of Im1.3

ctt gat gaa agg aat gcc gca gcc gac gac aaa gcg tct gac ctg atc
 Leu Asp Glu Arg Asn Ala Ala Asp Asp Lys Ala Ser Asp Leu Ile
 10 gct caa atc gtc agg aga gga tgc tgt tcc cat cct gcc tgt aac gtg
 Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Ala Cys Asn Val
 aat aat cca cac att tgt ggt tga
 Asn Asn Pro His Ile Cys Gly

TABLE 96

DNA Sequence (SEQ ID NO:327) and Protein Sequence (SEQ ID NO:328) of Lv1.2

tct gat ggc agg aat act gca gcc aaa gtc aaa tat tct aag acg ccg
 Ser Asp Gly Arg Asn Thr Ala Ala Lys Val Lys Tyr Ser Lys Thr Pro
 gag gaa tgc tgt ccc aat cct ccc tgt ttc gcg aca aat tcg gat att
 Glu Glu Cys Cys Pro Asn Pro Pro Cys Phe Ala Thr Asn Ser Asp Ile
 20 tgt ggc gga aga cgc tgatgctcca ggaccctctg aaccacgacg t
 Cys Gly Gly Arg Arg

TABLE 97

DNA Sequence (SEQ ID NO:329) and Protein Sequence (SEQ ID NO:330) of Lv1.3

tct aat ggc agg aat gcc gca gcc aaa ttc aaa gcg cct gcc ctg atg
 Ser Asn Gly Arg Asn Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 aag cgg acc gtc agg gat gct tgc tgt tca gac cct cgc tgt tcc ggg
 Lys Arg Thr Val Arg Asp Ala Cys Cys Ser Asp Pro Arg Cys Ser Gly
 aaa cat caa gac ctg tgt ggc tgaagacgct gatgctccag gaccctctga
 Lys His Gln Asp Leu Cys Gly
 30 accacgacgt

TABLE 98

DNA Sequence (SEQ ID NO:331) and Protein Sequence (SEQ ID NO:332) of Lv1.4

tct aat ggc agg aat gcc gca gcc aaa ttc aaa gcg cct gcc ctg atg
 Ser Asn Gly Arg Asn Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 gag ctg acc gtc agg gaa gat tgc tgt tca gac cct cgc tgt tcc gtg
 Glu Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val
 35

58

gga cat caa gac ctg tgt ggc tgaagacgct gatgctccag gaccctctga
 Gly His Gln Asp Leu Cys Gly
 accacgacgt

TABLE 99

5 DNA Sequence (SEQ ID NO:333) and Protein Sequence (SEQ ID NO:334) of Lv1.6

gca ttt gat ggc agg aat gct gca gcc agc gac aaa gcg tcc gag ctg
 Ala Phe Asp Gly Arg Asn Ala Ala Ser Asp Lys Ala Ser Glu Leu
 atg gct ctg gcc gtc agg gga tgc tgt tcc cat cct gcc tgg gct ggg
 Met Ala Leu Ala Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly
 10 agt aat gca cat atc tgt ggc aga aga cgc tgatgctcca ggaccctctg
 Ser Asn Ala His Ile Cys Gly Arg Arg Arg
 aaccacgacgt t

TABLE 100

DNA Sequence (SEQ ID NO:335) and Protein Sequence (SEQ ID NO:336) of Lv1.7

15 tct aat ggc agg aat gcc gca gcc aaa ttc aaa gcg cct gcc ctg atg
 Ser Asn Gly Arg Asn Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 aag ctg acc gtc agg gag gat tgc tgt tca gac cct cgc tgg tcc gtg
 Lys Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val
 20 gga cat caa gac atg tgt ggc tgaagacgct gatgctccag gaccctctga
 Gly His Gln Asp Met Cys Gly
 atcacgacgt

TABLE 101

DNA Sequence (SEQ ID NO:337) and Protein Sequence (SEQ ID NO:338) of Lv1.8

25 ttt gaa tgc agg aat gct gca ggc aac gac aaa gcg act gac ctg atg
 Phe Glu Cys Arg Asn Ala Ala Gly Asn Asp Lys Ala Thr Asp Leu Met
 gct ctg act gtc agg gga tgc tgt tcc cat cct gcc tgg gct ggg aat
 Ala Leu Thr Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn
 aat cca cat atc tgc ggc tgaagacgct gatgctccag gaccctctga
 Asn Pro His Ile Cys Gly
 30 accacgacgt

TABLE 102

DNA Sequence (SEQ ID NO:339) and Protein Sequence (SEQ ID NO:340) of Lv1.9

ttt gat ggc agg aac gcc gca gcc aac aac aaa gcg act gat ctg atg
 Phe Asp Gly Arg Asn Ala Ala Asn Asn Lys Ala Thr Asp Leu Met
 35 gct ctg act gtc agg gga tgc tgt ggc aat cct tca tgg agc atc cat
 Ala Leu Thr Val Arg Gly Cys Cys Gly Asn Pro Ser Cys Ser Ile His

59

att cct tac gtt tgt aat tagagacact gatgctccag gaccctctga
 Ile Pro Tyr Val Cys Asn
 accacgacgt

TABLE 103

5 DNA Sequence (SEQ ID NO:341) and Protein Sequence (SEQ ID NO:342) of Lv1.10

tct aat ggc agg aat gcc gca gcc aaa ttc aaa gcg cct gcc ctg atg
 Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 aag cgg acc gac agc gaa gaa tgc tgt tta gac tct cgc tgt gcc ggg
 Lys Arg Thr Asp Ser Glu Glu Cys Cys Leu Asp Ser Arg Cys Ala Gly
 10 caa cat caa gac ctg tgt ggc gga aga cgc tgatgctcca ggaccctctg
 Gln His Gln Asp Leu Cys Gly Gly Arg Arg
 aaccacgacgt t

TABLE 104

DNA Sequence (SEQ ID NO:343) and Protein Sequence (SEQ ID NO:344) of Mr1.3

15 tct gat ggc agg aat gcc gca gcc aag gac aaa gcg tct gac ctg gtc
 Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
 gct ctg acc gtc aag gga tgc tgt tct aat cct ccc tgt tac gcg aat
 Ala Leu Thr Val Lys Gly Cys Cys Ser Asn Pro Pro Cys Tyr Ala Asn
 aat caa gcc tat tgt aat gga aga cgc tga
 20 Asn Gln Ala Tyr Cys Asn Gly Arg Arg

TABLE 105

DNA Sequence (SEQ ID NO:345) and Protein Sequence (SEQ ID NO:346) of Mr1.4

tct gat ggc agg aat gcc gca gcc aag gac aaa gcg tct gac ctg gtc
 Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
 25 gct ctg acc gtc aag gga tgc tgt tct cat cct gcc tgt agc gtg aat
 Ala Leu Thr Val Lys Gly Cys Cys Ser His Pro Ala Cys Ser Val Asn
 aat cca gac att tgt ggt tga
 Asn Pro Asp Ile Cys Gly

TABLE 106

30 DNA Sequence (SEQ ID NO:347) and Protein Sequence (SEQ ID NO:348) of Ms1.1

tct gat ggc agg aat gct gca gcc aac aac aaa gtg gct ttg acc atg
 Ser Asp Gly Arg Asn Ala Ala Ala Asn Asn Lys Val Ala Leu Thr Met
 agg gga aaa tgc tgt atc aat gat gcg tgt cgc tcg aaa cat cca cag
 Arg Gly Lys Cys Ile Asn Asp Ala Cys Arg Ser Lys His Pro Gln
 35 tac tgt tct gga aga cgc tgatactcca ggaccctctg aaccacgacgt t
 Tyr Cys Ser Gly Arg Arg

TABLE 107

DNA Sequence (SEQ ID NO:349) and Protein Sequence (SEQ ID NO:350) of Ms1.6

tct gat ggc agg aat gct gca gcc aac gac aaa gtg tct gac cag atg
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Val Ser Asp Gln Met

5 gct ctg gtt gtc agg gga tgc tgt tac aat att gcc tgt aga att aat
 Ala Leu Val Val Arg Gly Cys Cys Tyr Asn Ile Ala Cys Arg Ile Asn

 aat cca cgg tac tgt cgt gga aaa cgc tgatgttcca ggaccctctg
 Asn Pro Arg Tyr Cys Arg Gly Lys Arg

 aaccacgacq t

10

TABLE 108

DNA Sequence (SEQ ID NO:351) and Protein Sequence (SEQ ID NO:352) of O1.1

tctgaaggca ggaatgccgc agccaacgac aaagcgtctg acctgatggc t ctg aac
Leu Asn

15 gtc agg gga tgc tgt tcc cat cct gtc tgt cgc ttc aat tat cca aaa
 Val Arg Gly Cys Cys Ser His Pro Val Cys Arg Phe Asn Tyr Pro Lys
 tat tgt ggt gga aga cgc tgatggtcca ggaccctctg aaccacgacg t
 Tyr Cys Gly Gly Arg Arg

TABLE 109

DNA Sequence (SEQ ID NO:353) and Protein Sequence (SEQ ID NO:354) of O1.2

20 tctgatggcg ggaatgccgc agcaaaagcg tttgatctaa tcact ctg gcc ctc agg
Leu Ala Leu Arg

gat gaa tgc tgt gcc agt cct ccc tgt cgt ttg aat aat cca tac gta
Asp Glu Cys Cys Ala Ser Pro Pro Cys Arg Leu Asn Asn Pro Tyr Val

25 tgt cat tgacgacgct gatgctccag gaccctctga accacgacgct
Cys His

TABLE 110

DNA Sequence (SEQ ID NO:355) and Protein Sequence (SEQ ID NO:356) of O1.4

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc acc gtc gtt tcc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

30 ccc act tca gat cgt gca tct gat agg agg aat gcc gca gcc aaa gcg
 Pro Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Ala Lys Ala
 ttt gac ctg aga tat tcg acc gcc aag aga gga tgc tgt tcc aat cct
 Phe Asp Leu Arg Tyr Ser Thr Ala Lys Arg Gly Cys Cys Ser Asn Pro
 35 gtc tgt tgg cag aat aat gca gaa tac tgt cgt gaa agt ggc
 Val Cys Trp Gln Asn Asn Ala Glu Tyr Cys Arg Glu Ser Gly

TABLE 111

DNA Sequence (SEQ ID NO:357) and Protein Sequence (SEQ ID NO:358) of O1.7

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 5
 ttc act tca gat cgt gca tct gat ggc ggg aat gtc gca gcg tct cac
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Val Ala Ala Ser His
 ctg atc gct ctg acc atc aag gga tgc tgt tct cac cct ccc tgt gcc
 Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala
 10
 cag aat aat caa gac tat tgt ggt tgacgacgct gatgctccag gaccctctga
 Gln Asn Asn Gln Asp Tyr Cys Gly
 accacgacgt

TABLE 112

DNA Sequence (SEQ ID NO:359) and Protein Sequence (SEQ ID NO:360) of O1.8

atg ttc acc gtg ttt ctg ttg gtc tta tca acc acc gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ser Thr Thr Val Val Ser
 15
 tcc act tca gat cgt gca tct gat agg agg aat gcc gca gcc aaa gcg
 Ser Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Lys Ala
 tct gac ctg atg tat tcg acc gtc aag aaa gga tgt tgt tcc cat cct
 Ser Asp Leu Met Tyr Ser Thr Val Lys Lys Gly Cys Cys Ser His Pro
 20
 gcc tgt tcg ggg aat aat cga gaa tat tgt cgt gaa agt ggc
 Ala Cys Ser Gly Asn Asn Arg Glu Tyr Cys Arg Glu Ser Gly
 taatgctcca ggaccctctg aaccacgacg t

TABLE 113

DNA Sequence (SEQ ID NO:361) and Protein Sequence (SEQ ID NO:362) of Om1.2

tttgatggca ggaatgcctc agccgacagc aaagtggctg cccggatcgc t cag atc
 Gln Ile
 25
 gac agg gat cca tgc tgt tcc tat cct gac tgt ggc gcg aat cat cca
 Asp Arg Asp Pro Cys Cys Ser Tyr Pro Asp Cys Gly Ala Asn His Pro
 gag att tgt ggt gga aaa cgc tcatgctcca ggaccctctg aaccacgacg t
 Glu Ile Cys Gly Lys Arg
 30

TABLE 114

DNA Sequence (SEQ ID NO:363) and Protein Sequence (SEQ ID NO:364) of Om1.3

tctcatggca ggaatgccgc acgct ctg acc gtc agg gaa tgc tgt tct cag
 Leu Thr Val Arg Glu Cys Cys Ser Gln
 35
 cct cct tgt cgc tgg aaa cat cca gaa ctt tgt agt tgaagacgct
 Pro Pro Cys Arg Trp Lys His Pro Glu Leu Cys Ser

62

gatgctccag gaccctctga accacgacgt

TABLE 115

DNA Sequence (SEQ ID NO:365) and Protein Sequence (SEQ ID NO:366) of Om1.4

5

tttcatggca ggaatgctgc agccagcgac aaagcgtctg agctgatggc t ctg gcc
Leu Ala
gtc agg gga tgc tgt tcc cat cct gcc tgt gct ggg aat aat cca cat
Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn Asn Pro His
atc tgt ggc aga aga cgc tgatgctcca ggaccctctg aaccacgacgt t
Ile Cys Gly Arg Arg

10

TABLE 116

DNA Sequence (SEQ ID NO:367) and Protein Sequence (SEQ ID NO:368) of Om1.5

15

tctggtgtca ggaaagacgc agcgctggc ctgatcgct ctg acc atc aag gga
Leu Thr Ile Lys Gly
tgc tgt tct gat cct agc tgt aac gtg aat aat cca gac tat tgt ggt
Cys Cys Ser Asp Pro Ser Cys Asn Val Asn Asn Pro Asp Tyr Cys Gly
tgacgacgt gatgctccag gaccctctga accacgacgt

TABLE 117

DNA Sequence (SEQ ID NO:369) and Protein Sequence (SEQ ID NO:370) of Om1.6

20

tctaattggca ggaatgccgc agccaaattc aaagcgcttg ccctgatgg a g ctg acc 57
Leu Thr
gtc agg gaa gaa tgc tgt tca gac cct cgc tgt tcc gtg gga cat caa 105
Val Arg Glu Glu Cys Cys Ser Asp Pro Arg Cys Ser Val Gly His Gln
gat atg tgt cgg tgaaggcacgt gatgctccag gaccctctga accacgacgt 157
Asp Met Cys Arg

25

TABLE 118

DNA Sequence (SEQ ID NO:371) and Protein Sequence (SEQ ID NO:372) of P1.4

30

act gat ggc agg aat gct gca gcc ata gcg ctt gac ctg atc gct ccg
Thr Asp Gly Arg Asn Ala Ala Ala Ile Ala Leu Asp Leu Ile Ala Pro
gcc gtc agg gga gga tgc tgt tcc aat cct gcc tgt tta gtg aat cat
Ala Val Arg Gly Gly Cys Cys Ser Asn Pro Ala Cys Leu Val Asn His
cta gaa atg tgt ggt aaa aga cgc tgatgccccca ggaccctctg aaccacgacgt
Leu Glu Met Cys Gly Lys Arg Arg
t

TABLE 119

DNA Sequence (SEQ ID NO:373) and Protein Sequence (SEQ ID NO:374) of P1.5

tct gat ggc agg gat gcc gca gcc aac gac aaa gcg tct gac ctg atc
 Ser Asp Gly Arg Asp Ala Ala Asn Asp Lys Ala Ser Asp Leu Ile
 5 gct ctg acc gcc agg aga gat cca tgc tgt ttc aat cct gcc tgt aac
 Ala Leu Thr Ala Arg Arg Asp Pro Cys Cys Phe Asn Pro Ala Cys Asn
 gtg aat aat cca cag att tgt ggt tgaagacgct gatgctccag gaccctctga
 Val Asn Asn Pro Gln Ile Cys Gly
 accacgacgt

10

TABLE 120

DNA Sequence (SEQ ID NO:375) and Protein Sequence (SEQ ID NO:376) of P1.6

tct gat ggc agg gat gct gag aaa aca ggc ttt gac acg acc att gtg
 Ser Asp Gly Arg Asp Ala Glu Lys Thr Gly Phe Asp Thr Thr Ile Val
 15 ccg gaa gac tgc tgt tcg gat cct tcc tgt tgg agg ctg cat agt tta
 Pro Glu Asp Cys Cys Ser Asp Pro Ser Cys Trp Arg Leu His Ser Leu
 gct tgt act gga att gta aac cgc tgatgctcca ggaccctctg aaccacgacg
 Ala Cys Thr Gly Ile Val Asn Arg
 t

TABLE 121

20

DNA Sequence (SEQ ID NO:377) and Protein Sequence (SEQ ID NO:378) of P1.8

act gat ggc agg agt gct gca gcc ata gcg ttt gcc ctg atc gct ccg
 Thr Asp Gly Arg Ser Ala Ala Ile Ala Phe Ala Leu Ile Ala Pro
 acc gtc tgc tgt act aat cct gcc tgt ctc gtg aat aat ata cgc ttt
 Thr Val Cys Cys Thr Asn Pro Ala Cys Leu Val Asn Asn Ile Arg Phe
 25 tgt ggt gga aga cgc tgatgccccca ggaccctctg aaccacgacg t
 Cys Gly Arg Arg

TABLE 122

DNA Sequence (SEQ ID NO:379) and Protein Sequence (SEQ ID NO:380) of Rg1.1

30

tct gat gga aga aat gcc gca agc gac gcc aaa gcg ttt ccc cgg atc
 Ser Asp Gly Arg Asn Ala Ala Ser Asp Ala Lys Ala Phe Pro Arg Ile
 gct cca atc gtc agg gac gaa tgc tgt agc gat cct agg tgt cac ggg
 Ala Pro Ile Val Arg Asp Glu Cys Cys Ser Asp Pro Arg Cys His Gly
 aat aat cgg gac cac tgt gct tgaagacgct gatgctccag gaccctctga
 Asn Asn Arg Asp His Cys Ala
 35 accacgacgt

64

TABLE 123

DNA Sequence (SEQ ID NO:381) and Protein Sequence (SEQ ID NO:382) of Rg1.3

tct gat ggc agg aat acc gca gcc gac aac aaa gca tcc gac ctc atc
 Ser Asp Gly Arg Asn Thr Ala Ala Asp Glu Lys Ala Ser Asp Leu Ile
 5 tct caa act gtc aag aga gat tgc tgt tcc cat cct ctc tgt aga tta
 Ser Gln Thr Val Lys Arg Asp Cys Ser His Pro Leu Cys Arg Leu
 ttt gtt cca gga ctt tgt att tgaagacgct gctgctccag gaccctctga
 Phe Val Pro Gly Leu Cys Ile
 accacgact

10

TABLE 124

DNA Sequence (SEQ ID NO:383) and Protein Sequence (SEQ ID NO:384) of Rg1.4

tct gat ggc agg aat gcc gca gcc gac aac aaa gca tct gac cta atc
 Ser Asp Gly Arg Asn Ala Ala Asp Asn Lys Ala Ser Asp Leu Ile
 15 gct caa atc gtc agg aga gga tgc tgt tcc cat cct gtc tgt aaa gtg
 Ala Gln Ile Val Arg Arg Gly Cys Ser His Pro Val Cys Lys Val
 agg tat cca gac ctg tgt cgt tgaagacgct gctgctccag gaccctctga
 Arg Tyr Pro Asp Leu Cys Arg
 accacgacgt

20

TABLE 125

DNA Sequence (SEQ ID NO:385) and Protein Sequence (SEQ ID NO:386) of Rg1.5

tct gat ggc agg aat gcc gca gcc gac aac aga gca tct gac cta atc
 Ser Asp Gly Arg Asn Ala Ala Asp Asn Arg Ala Ser Asp Leu Ile
 gct caa atc gtc agg aga gga tgc tgt tcc cat cct gcc tgt aat gtg
 Ala Gln Ile Val Arg Arg Gly Cys Ser His Pro Ala Cys Asn Val
 25 aat aat cca cac att tgt ggt tgaagacgct gctgctccag gaccctctga
 Asn Asn Pro His Ile Cys Gly
 accacgacgt

TABLE 126

DNA Sequence (SEQ ID NO:387) and Protein Sequence (SEQ ID NO:388) of Rg1.8

tct gat ggc agg aat gcc gca gcc gac aac aaa ccg tct gac cta atc
 Ser Asp Gly Arg Asn Ala Ala Asp Asn Lys Pro Ser Asp Leu Ile
 gct caa atc gtc agg aga gga tgc tgt tcg cat cct gtc tgt aaa gtg
 Ala Gln Ile Val Arg Arg Gly Cys Ser His Pro Val Cys Lys Val
 35 agg tat tca gac atg tgt ggt tgaagacgct gctgctccag gaccctctga
 Arg Tyr Ser Asp Met Cys Gly
 accacgacgt

TABLE 127

DNA Sequence (SEQ ID NO:389) and Protein Sequence (SEQ ID NO:390) of Sm1.4

tct gat ggc agg aat gca gag cga cga caa agc gtc tgt cct ggt cgc
 Ser Asp Gly Arg Asn Ala Glu Arg Arg Gln Ser Val Cys Pro Gly Arg
 5 tct ggc ccc agg gga gga tgt tgt tcc cac cct gcc tgt aag gtg cat
 Ser Gly Pro Arg Gly Gly Cys Cys Ser His Pro Ala Cys Lys Val His
 ttt cca cac agt tgt ggt tgacgacgct gatgctccag gaccctctga
 Phe Pro His Ser Cys Gly
 accacgacgt

10

TABLE 128

DNA Sequence (SEQ ID NO:391) and Protein Sequence (SEQ ID NO:392) of Sm1.5

tct gat ggc agg aat gcc gca gcc agc gac aga gcg tct gac gcg gcc
 Ser Asp Gly Arg Asn Ala Ala Ser Asp Arg Ala Ser Asp Ala Ala
 15 cac cag gta tgc tgt tcc aac cct gtc tgt cac gtg gat cat cca gaa
 His Gln Val Cys Cys Ser Asn Pro Val Cys His Val Asp His Pro Glu
 ctt tgt cgt aga aga cgc tgatgctcca ggaccctctg aaccacgacg t
 Leu Cys Arg Arg Arg

TABLE 129

DNA Sequence (SEQ ID NO:393) and Protein Sequence (SEQ ID NO:394) of S1.5

20 tct gat ggc agg aat gcc gcg gcc aac gac aaa gcg tct gac ctg gtc
 Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Ala Ser Asp Leu Val
 gct ccg gcc atc agg gga tgc tgt tcc cac cct gtc tgt aac ttg agt
 Ala Pro Ala Ile Arg Gly Cys Cys Ser His Pro Val Cys Asn Leu Ser
 25 aat cca caa att tgt cgt gga aga cgc tgatgctcca ggaccctctg
 Asn Pro Gln Ile Cys Arg Gly Arg Arg
 aaccacgacg t

TABLE 130

DNA Sequence (SEQ ID NO:395) and Protein Sequence (SEQ ID NO:396) of Tx1.5

30 ttt cat ggc agg aat gcc gca gcc aaa gcg tct ggc ctg gtc ggt ctg
 Phe His Gly Arg Asn Ala Ala Lys Ala Ser Gly Leu Val Gly Leu
 acc gac aag agg caa gaa tgc tgt tct cat cct gcc tgt aac gta gat
 Thr Asp Lys Arg Gln Glu Cys Cys Ser His Pro Ala Cys Asn Val Asp
 cat cca gaa att tgt cgt tga
 His Pro Glu Ile Cys Arg

TABLE 131

DNA Sequence (SEQ ID NO:397) and Protein Sequence (SEQ ID NO:398) of T1.1

act gat ggc agg agt gct gca gcc ata gcg ttt gcc ctg atc gct ccg
 Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala Phe Ala Leu Ile Ala Pro

5 acc gtc tgg gaa gga tgc tgt tct aat cct gcc tgt ctc gtg aat cat
 Thr Val Trp Glu Gly Cys Ser Asn Pro Ala Cys Leu Val Asn His

ata cgc ttt tgt ggt gga aga cgc tgatgccccca ggaccctctg aaccacgacg
 Ile Arg Phe Cys Gly Arg Arg

t

10

TABLE 132

DNA Sequence (SEQ ID NO:399) and Protein Sequence (SEQ ID NO:400) of Vr1.3

tct aat ggc atg aat gcc gca gcc atc agg aaa gcg tct gcc ctg gtg
 Ser Asn Gly Met Asn Ala Ala Ile Arg Lys Ala Ser Ala Leu Val

15 gct cag atc gcc cat cga gac tgc tgt gac gat cct gcc tgc acc gtg
 Ala Gln Ile Ala His Arg Asp Cys Cys Asp Asp Pro Ala Cys Thr Val

aat aat cca ggc ctt tgc act tgaagatgct gctgccccag gaccctctga
 Asn Asn Pro Gly Leu Cys Thr

accacgacgt

TABLE 133

20

DNA Sequence (SEQ ID NO:401) and Protein Sequence (SEQ ID NO:402) of G1.2

tct gat ggc ggg aat gcc gca gca aaa gag tct gac gtg atc gct ctg
 Ser Asp Gly Gly Asn Ala Ala Lys Glu Ser Asp Val Ile Ala Leu

acc gtc tgg aaa tgc tgt acc att cct tcc tgt tat gag aaa aaa aaa
 Thr Val Trp Lys Cys Cys Thr Ile Pro Ser Cys Tyr Glu Lys Lys

25

att aaa gca tgt gtc ttt tgacgacgct gatgctccag gaccctctga
 Ile Lys Ala Cys Val Phe

accacgacgt

TABLE 134

DNA Sequence (SEQ ID NO:403) and Protein Sequence (SEQ ID NO:404) of Rg1.12

30

tct gat ggc gca gtc gac gac aaa gcg ttg gat cga atc gct gaa atc
 Ser Asp Gly Ala Val Asp Asp Lys Ala Leu Asp Arg Ile Ala Glu Ile

gtc agg aga gga tgc tgt ggc aat cct gcc tgt agc ggc tcc tcg aaa
 Val Arg Arg Gly Cys Cys Gly Asn Pro Ala Cys Ser Gly Ser Ser Lys

35

gat gca ccc tct tgt ggt tgaagacgct gctgctccag gaccctctga
 Asp Ala Pro Ser Cys Gly

accacgacgt

It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

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WHAT IS CLAIMED IS:

1. A substantially pure α -conotoxin peptide having the generic formula I: Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Cys-Cys-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Cys-Xaa₁₀-Xaa₁₁-Xaa₁₂-Cys-Xaa₁₃ (SEQ ID NO1:), wherein Xaa₁ is des-Xaa₁, Ile, Leu or Val; Xaa₂ is des-Xaa₂, Ala or Gly; Xaa₃ is des-Xaa₃, Gly, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa₄ is des-Xaa₄, Asp, Phe, Gly, Ala, Glu, γ -carboxy-Glu (Gla) or any unnatural aromatic amino acid; Xaa₅ is Glu, Gla, Asp, Ala, Thr, Ser, Gly, Ile, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₆ is Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₇ is Asp, Glu, Gla, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₈ is Ser, Thr, Asn, Ala, Gly, His, halo-His, Pro or hydroxy-Pro; Xaa₉ is Thr, Ser, Ala, Asp, Asn, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₀ is Gly, Ser, Thr, Ala, Asn, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₁ is Gln, Leu, His, halo-His, Trp (D or L), halo-Trp, neo-Trp, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa₁₂ is Asn, His, halo-His, Ile, Leu, Val, Gln, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₃ is des-Xaa₁₃, Val, Ile, Leu, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; and the C-terminus contains a free carboxyl group or an amide group.
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2. A substantially pure α -conotoxin peptide of generic formula I selected from the group consisting of:
Asp-Xaa₁-Cys-Cys-Ser-Asp-Ser-Arg-Cys-Gly-Xaa₂-Asn-Cys-Leu (SEQ ID NO:4);
Ala-Cys-Cys-Ser-Asp-Arg-Arg-Cys-Arg-Xaa₃-Arg-Cys (SEQ ID NO:5);
Phe-Thr-Cys-Cys-Arg-Arg-Gly-Thr-Cys-Ser-Gln-His-Cys (SEQ ID NO:6);
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Asp-Xaa₄-Cys-Cys-Arg-Arg-His-Ala-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:7);
Asp-Xaa₄-Cys-Cys-Arg-Xaa₅-Xaa₆-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:8);
Gly-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Arg-Xaa₄-Arg-Cys-Arg (SEQ ID NO:9);
Gly-Gly-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ala-Xaa₆-Arg-Cys (SEQ ID NO:10);
Ile-Ala-Xaa₅-Asp-Ile-Cys-Cys-Ser-Xaa₆-Xaa₇-Asp-Cys-Asn-His-Xaa₂-Cys-Val(SEQ
ID NO:11); and
Gly-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Xaa₂-His-Gln-Cys (SEQ ID NO:12),
wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys
10 or N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or
hydroxy-Pro; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

3. The substantially pure α -conotoxin peptide of claim 2, wherein Xaa₁ is Glu.
4. The substantially pure α -conotoxin peptide of claim 2, wherein Xaa₂ is Lys.
5. The substantially pure α -conotoxin peptide of claim 2, wherein Xaa₄ is Tyr.
- 15 6. The substantially pure α -conotoxin peptide of claim 2, wherein Xaa₄ is mono-iodo-Tyr.
7. The substantially pure α -conotoxin peptide of claim 2, wherein Xaa₄ is di-iodo-Tyr.
8. The substantially pure α -conotoxin peptide of claim 1, which is modified to contain an O-glycan, an S-glycan or an N-glycan.
9. The substantially pure α -conotoxin peptide of claim 2 which is modified to contain an O-glycan, an S-glycan or an N-glycan.
- 20 10 A substantially pure α -conotoxin peptide having the generic formula II: Xaa₁-Xaa₂-Xaa₃-Xaa₄-Cys-Cys-Xaa₅-Xaa₆-Xaa₇-Xaa₈-Cys-Xaa₉-Xaa₁₀-Xaa₁₁-Xaa₁₂-Xaa₁₃-Xaa₁₄-Cys-Xaa₁₅-Xaa₁₆-Xaa₁₇, (SEQ ID NO:2), wherein Xaa₁ is des-Xaa₁, Asp, Glu or γ -carboxy-Glu (Gla);

Xaa₂ is des-Xaa₂, Gln, Ala, Asp, Glu, Gla; Xaa₃ is des-Xaa₃, Gly, Ala, Asp, Glu, Gla, Pro or hydroxy-Pro; Xaa₄ is des-Xaa₄, Gly, Glu, Gla, Gln, Asp, Asn, Pro or hydroxy-Pro; Xaa₅ is Ser, Thr, Gly, Glu, Gla, Asn, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₆ is Asp, Asn, His, halo-His, Thr, Ser, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₇ is Pro or hydroxy-Pro; Xaa₈ is Ala, Ser, Thr, Asp, Val, Ile, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₉ is Gly, Ile, Leu, Val, Ala, Thr, Ser, Pro, hydroxy-Pro, Phe, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa₁₀ is Ala, Asn, Phe, Pro, hydroxy-Pro, Glu, Gla, Gln, His, halo-His, Val, Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₁ is Thr, Ser, His, halo-His, Leu, Ile, Val, Asn, Met, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₂ is Asn, Pro, hydroxy-Pro, Gln, Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₃ is des-Xaa₁₃, Gly, Thr, Ser, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₄ is des-Xaa₁₄, Ile, Val, Asp, Leu, Phe, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; and Xaa₁₅ is des-Xaa₁₅, Gly, Ala, Met, Ser, Thr, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₆ is des-Xaa₁₆, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-

Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₇ is Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₇ is des-Xaa₁₇, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; and the C-terminus contains a free carboxyl group or an amide group.

- 5 11. A substantially pure α -conotoxin peptide of generic formula II selected from the group consisting of:
- Cys-Cys-Ser-Asp-Xaa₅-Ala-Cys-Xaa₂-Gln-Thr-Xaa₅-Gly-Cys-Arg (SEQ ID NO:13);
Cys-Cys-Xaa₅-Asn-Xaa₅-Ala-Cys-Arg-His-Thr-Gln-Gly-Cys (SEQ ID NO:14);
Gly-Cys-Cys-Xaa₅-His-Xaa₅-Ala-Cys-Gly-Arg-His-Xaa₄-Cys (SEQ ID NO:15);
10 Ala-Xaa₅-Cys-Cys-Asn-Asn-Xaa₅-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:16);
Ala-Xaa₅-Gly-Cys-Cys-Asn-Asn-Xaa₅-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:17);
NO:17);
Xaa₅-Xaa₅-Cys-Cys-Asn-Asn-Xaa₅-Ala-Cys-Val-Xaa₂-His-Arg-Cys (SEQ ID NO:18);
15 Asp-Xaa₅-Asn-Cys-Cys-Xaa₅-Asn-Xaa₅-Ser-Cys-Xaa₅-Arg-Xaa₅-Arg-Cys-Thr (SEQ ID NO:19);
ID NO:19);
Gly-Cys-Cys-Ser-Thr-Xaa₅-Xaa₅-Cys-Ala-Val-Leu-Xaa₄-Cys (SEQ ID NO:20);
Gly-Cys-Cys-Gly-Asn-Xaa₅-Asp-Cys-Thr-Ser-His-Ser-Cys (SEQ ID NO:21);
Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₅-Cys-Ala-His-Asn-Asn-Xaa₅-Asp-Cys-Arg (SEQ
20 ID NO:42);
Gly-Cys-Cys-Xaa₄-Asn-Xaa₅-Val-Cys-Xaa₂-Xaa₂-Xaa₄-Cys-Xaa₃-Xaa₂ (SEQ
ID NO:154);
Xaa₆-Xaa₁-Xaa₅-Gly-Cys-Cys-Arg-His-Xaa₅-Ala-Cys-Gly-Xaa₂-Asn-Arg-Cys (SEQ
ID NO:155);
25 Cys-Cys-Ala-Asp-Xaa₅-Asp-Cys-Arg-Phe-Arg-Xaa₅-Gly-Cys (SEQ ID NO:156);
Gly-Cys-Cys-Xaa₄-Asn-Xaa₅-Ser-Cys-Xaa₃-Xaa₅-Xaa₂-Thr-Xaa₄-Cys-Ser-Xaa₃-Xaa₂
(SEQ ID NO:157);
Cys-Cys-Ser-Asn-Xaa₅-Thr-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:158);
Cys-Cys-Ala-Asn-Xaa₅-Ile-Cys-Xaa₂-Asn-Thr-Xaa₅-Gly-Cys (SEQ ID NO:159);
Cys-Cys-Asn-Asn-Xaa₅-Thr-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:160);
30 Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-Xaa₂-Xaa₁-Thr-Xaa₄-Gly-Cys (SEQ ID NO:161);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₃-Xaa₂-Cys-Ile-Ala-Ser-Asn-Xaa₅-Xaa₂-Cys-Gly (SEQ ID NO:162);

5 Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Ser-Ala-Met-Ser-Xaa₅-Ile-Cys (SEQ ID NO:163);

Gly-Cys-Cys-Xaa₂-Asn-Xaa₃-Xaa₄-Cys-Gly-Ala-Ser-Xaa₂-Thr-Xaa₄-Cys (SEQ ID NO:164);

10 Gly-Cys-Cys-Ser-Xaa₄-Xaa₃-Xaa₅-Cys-Phe-Ala-Thr-Asn-Xaa₅-Asp-Cys (SEQ ID NO:165);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₃-Xaa₅-Cys-Ile-Ala-Asn-Asn-Xaa₅-Leu-Cys-Ala (SEQ ID NO:166);

15 Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₃-Xaa₅-Cys-Ile-Ala-Asn-Asn-Xaa₅-Phe-Cys-Ala (SEQ ID NO:167);

Asp-Cys-Cys-Ser-Asn-Xaa₃-Xaa₅-Cys-Ser-Gln-Asn-Asn-Xaa₅-Asp-Cys-Met (SEQ ID NO:168); and

20 15 Asp-Cys-Cys-Ser-Asn-Xaa₃-Xaa₅-Cys-Ala-His-Asn-Asn-Xaa₅-Asp-Cys-Arg (SEQ ID NO:169),

wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

12. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₂ is Lys.
13. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₁ is Glu.
14. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₃ is Trp.
15. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₄ is Tyr.
- 25 16. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₄ is mono-iodo-Tyr.
17. The substantially pure α -conotoxin peptide of claim 11, wherein Xaa₄ is di-iodo-Tyr.

18. The substantially pure α -conotoxin peptide of claim 10, which is modified to contain an O-glycan, an S-glycan or an N-glycan.
19. The substantially pure α -conotoxin peptide of claim 11 which is modified to contain an O-glycan, an S-glycan or an N-glycan.
- 5 20. A substantially pure α -conotoxin peptide having the generic formula III: Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Cys-Cys-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Cys-Xaa₁₀-Xaa₁₁-Xaa₁₂-Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Cys-Xaa₁₇-Xaa₁₈-Xaa₁₉-Xaa₂₀-Xaa₂₁-Xaa₂₂-Xaa₂₃-Xaa₂₄ (SEQ ID NO:3), wherein Xaa₁ is des-Xaa₁, Ser or Thr; Xaa₂ is des-Xaa₂, Asp, Glu, γ -carboxy-Glu (Gla), Asn, Ser or Thr; Xaa₃ is des-Xaa₃, Ala, Gly, Asn, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₄ is des-Xaa₄, Ala, Val, Leu, Ile, Gly, Glu, Gla, Gln, Asp, Asn, Phe, Pro, hydroxy-Pro or any unnatural aromatic amino acid; Xaa₅ is des-Xaa₅, Thr, Ser, Asp, Glu, Gla, Gln, Gly, Val, Asp, Asn, Ala, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₆ is Thr, Ser, Asp, Asn, Met, Val, Ala, Gly, Leu, Ile, Phe, any unnatural aromatic amino acid, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₇ is Ile, Leu, Val, Ser, Thr, Gln, Asn, Asp, Arg, His, halo-His, Phe, any unnatural aromatic amino acid, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₈ is Pro, hydroxy-Pro, Ser, Thr, Ile, Asp, Leu, Val, Gly, Ala, Phe, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₉ is Val, Ala, Gly, Ile, Leu, Asp, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₀ is His, halo-His, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Asn, Ala, Ser, Thr, Phe, Ile, Leu, Gly, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₁ is Leu, Gln, Val, Ile,

Gly, Met, Ala, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Ser, Thr, Arg,
homoarginine, ornithine, any unnatural basic amino acid, Asn, Glu, Gla, Gln, Phe, Trp (D
or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa₁₂ is Glu, Gla, Gln, Asn,
Asp, Pro, hydroxy-Pro, Ser, Gly, Thr, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-
trimethyl-Lys, Arg, homoarginine, ornithine, any unnatural basic amino acid, Phe, His, halo-
His, any unnatural aromatic amino acid, Leu, Met, Gly, Ala, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing
amino acid; Xaa₁₃ is His, halo-His, Asn, Thr, Ser, Ile, Val, Leu, Phe, any unnatural aromatic
amino acid, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-
trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid;
Xaa₁₄ is Ser, Thr, Ala, Gln, Pro, hydroxy-Pro, Gly, Ile, Leu, Arg, ornithine, homoarginine,
Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino
acid; Xaa₁₅ is Asn, Glu, Gla, Asp, Gly, His, halo-His, Ala, Leu, Gln, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural
basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa₁₆ is Met, Ile, Thr, Ser, Val,
Leu, Pro, hydroxy-Pro, Phe, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-
Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, any unnatural hydroxy
containing amino acid, Glu, Gla, Ala, His, halo-His, Arg, ornithine, homoarginine, Lys, N-
methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid;
Xaa₁₇ is des-Xaa₁₇, Gly, Asp, Asn, Ala, Ile, Leu, Ser, Thr, His, halo-His, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid; Xaa₁₈ is des-Xaa₁₈, Gly, Glu, Gla, Gln, Trp (D or L), neo, halo-
Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₁₉ is des-
Xaa₁₉, Ser, Thr, Val, Ile, Ala, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-
dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₀ is des-Xaa₂₀,
Val, Asp, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-
Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₁ is des-Xaa₂₁, Asn, Pro
or hydroxy-Pro; Xaa₂₂ is des-Xaa₂₂, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-
dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa₂₃ is des-Xaa₂₃,

Ser or Thr; Xaa₂₄ is des-Xaa₂₄, Leu, Ile or Val; and the C-terminus contains a free carboxyl group or an amide group, with the proviso that (a) Xaa₅ is not Gly, when Xaa₁ is des-Xaa₁, Xaa₂ is des-Xaa₂, Xaa₃ is des-Xaa₃, Xaa₄ is des-Xaa₄, Xaa₆ is Ser, Xaa₇ is His, Xaa₈ is Pro, Xaa₉ is Ala, Xaa₁₀ is Ser, Xaa₁₁ is Val, Xaa₁₂ is Asn, Xaa₁₃ is Asn, Xaa₁₄ is Pro, Xaa₁₅ is Asp, Xaa₁₆ is Ile, Xaa₁₇ is des-Xaa₁₇, Xaa₁₈ is des-Xaa₁₈, Xaa₁₉ is des-Xaa₁₉, Xaa₂₀ is des-Xaa₂₀, Xaa₂₁ is des-Xaa₂₁, Xaa₂₂ is des-Xaa₂₂, Xaa₂₃ is des-Xaa₂₃, and Xaa₂₄ is des-Xaa₂₄.

21. A substantially pure α -conotoxin peptide of generic formula III selected from the group consisting of:

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Leu-Xaa₁-His-Ser-Asn-Met-Cys (SEQ ID NO:22);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-Arg-Gln-Asn-Asn-Ala-Xaa₁-Xaa₄-Cys-Arg (SEQ ID NO:23);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:24);

Xaa₅-Xaa₁-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:25);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Asp (SEQ ID NO:26);

Xaa₅-Arg-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:27);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Gly-Ile-Cys-Arg (SEQ ID NO:28);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Thr-Cys-Arg (SEQ ID NO:29);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Val-Cys-Arg (SEQ ID NO:30);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Ile-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:31);

Xaa₅-Gln-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg-Arg-Arg (SEQ ID NO:32);

Gly-Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Val-Asn-His-Xaa₁-Leu-Cys (SEQ ID NO:33);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Val-Asn-His-Xaa₁-Leu-Cys (SEQ ID NO:34);

5 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys (SEQ ID NO:35);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Gly-Xaa₂-Thr-Gln-Xaa₁-Xaa₃-Cys-Arg-Xaa₄-Ser (SEQ ID NO:36);

10 Xaa₅-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Gly-Asn-Asn-Xaa₅-Xaa₁-Phe-Cys-Arg-Gln (SEQ ID NO:37);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Gly-Asn-Asn-Xaa₅-Xaa₁-Phe-Cys-Arg-Gln (SEQ ID NO:38);

Gly-Cys-Cys-Ser-His-Xaa₅-Xaa₁-Cys-Ala-Met-Asn-Asn-Xaa₅-Asp-Xaa₄-Cys (SEQ ID NO:39);

15 Gly-Cys-Cys-Ser-His-Xaa₅-Xaa₁-Cys-Phe-Leu-Asn-Asn-Xaa₅-Asp-Xaa₄-Cys (SEQ ID NO:40);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₁-Cys-Ile-Ala-Xaa₂-Asn-Xaa₃-His-Met-Cys-Gly (SEQ ID NO:41);

20 Gly-Cys-Cys-Ser-Asn-Xaa₅-Ala-Cys-Ala-Gly-Asn-Asn-Xaa₅-His-Val-Cys-Arg-Gln (SEQ ID NO:43);

Gly-Cys-Cys-Ser-Arg-Xaa₅-Ala-Cys-Ile-Ala-Asn-Asn-Xaa₅-Asp-Leu-Cys (SEQ ID NO:44);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Val-Xaa₁-His-Xaa₃-Xaa₁-Leu-Cys-Arg-Arg-Arg (SEQ ID NO:45);

25 Gly-Gly-Cys-Cys-Ser-Phe-Xaa₅-Ala-Cys-Arg-Xaa₂-Xaa₅-Arg-Xaa₃-Xaa₁-Met-Cys-Gly (SEQ ID NO:46);

Xaa₅-Xaa₁-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Asn-Ser-Ser-His-Xaa₅-Xaa₁-Leu-Cys-Gly (SEQ ID NO:47);

30 Xaa₅-Gln-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Asn-Val-Gly-His-Xaa₅-Xaa₁-Leu-Cys-Gly (SEQ ID NO:48);

Xaa₆-Val-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Asn-Val-Gly-His-Xaa₅-Xaa₁-Ile-Cys-Gly (SEQ ID NO:49);

Gly-Cys-Cys-Ser-Arg-Xaa₅-Xaa₅-Cys-Ile-Ala-Asn-Asn-Xaa₅-Asp-Leu-Cys (SEQ ID NO:50);

Xaa₅-Gln-Cys-Cys-Ser-His-Leu-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:51);

5 Gly-Cys-Cys-Ser-Xaa₄-Phe-Asp-Cys-Arg-Met-Met-Phe-Xaa₅-Xaa₁-Met-Cys-Gly-Xaa₃-Arg (SEQ ID NO:52);

Gly-Gly-Cys-Cys-Ser-Phe-Ala-Ala-Cys-Arg-Xaa₂-Xaa₄-Arg-Xaa₅-Xaa₁-Met-Cys-Gly (SEQ ID NO:53);

10 Gly-Gly-Cys-Cys-Phe-His-Xaa₅-Val-Cys-Xaa₄-Ile-Asn-Leu-Leu-Xaa₁-Met-Cys-Arg-Gln-Arg (SEQ ID NO:54);

Ser-Ala-Thr-Cys-Cys-Asn-Xaa₄-Xaa₅-Xaa₅-Cys-Xaa₄-Xaa₁-Thr-Xaa₄-Xaa₅-Xaa₁-Ser-Cys-Leu (SEQ ID NO:55);

Ala-Cys-Cys-Ala-Xaa₄-Xaa₅-Xaa₅-Cys-Phe-Xaa₁-Ala-Xaa₄-Xaa₅-Xaa₁-Arg-Cys-Leu (SEQ ID NO:56);

15 Asn-Ala-Xaa₁-Cys-Cys-Xaa₄-Xaa₄-Xaa₅-Xaa₅-Cys-Xaa₄-Xaa₁-Ala-Xaa₄-Xaa₅-Xaa₁-Ile-Cys-Leu (SEQ ID NO:57);

Xaa₁-Cys-Cys-Thr-Asn-Xaa₅-Val-Cys-His-Ala-Xaa₁-His-Gln-Xaa₁-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:170);

20 Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Leu-Xaa₁-His-Ser-Asn-Leu-Cys (SEQ ID NO:171);

Xaa₁-Cys-Cys-Thr-Asn-Xaa₅-Val-Cys-His-Val-Xaa₁-His-Gln-Xaa₁-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:172);

25 Xaa₆-Xaa₁-Cys-Cys-Ser-Xaa₄-Xaa₅-Ala-Cys-Asn-Leu-Asp-His-Xaa₅-Xaa₁-Leu-Cys (SEQ ID NO:173);

Xaa₅-Xaa₁-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Asn-Ser-Thr-His-Xaa₅-Xaa₁-Leu-Cys-Gly (SEQ ID NO:174);

Leu-Asn-Cys-Cys-Met-Ile-Xaa₅-Xaa₅-Cys-Xaa₃-Xaa₂-Xaa₂-Xaa₄-Gly-Asp-Arg-Cys-Ser-Xaa₁-Val-Arg (SEQ ID NO:175);

30 Ala-Phe-Gly-Cys-Cys-Asp-Leu-Ile-Xaa₅-Cys-Leu-Xaa₁-Arg-Xaa₄-Gly-Asn-Arg-Cys-Asn-Xaa₁-Val-His (SEQ ID NO:176);

Leu-Gly-Cys-Cys-Asn-Val-Thr-Xaa₅-Cys-Xaa₃-Xaa₁-Xaa₂-Xaa₄-Gly-Asp-Xaa₂-Cys-Asn-Xaa₁-Val-Arg (SEQ ID NO:177);

Asp-Xaa,-Cys-Cys-Ser-Asn-Xaa,-Ala-Cys-Arg-Val-Asn-Asn-Xaa,-His-Val-Cys-
Arg-Arg-Arg (SEQ ID NO:178);

Leu-Asn-Cys-Cys-Ser-Ile-Xaa,-Gly-Cys-Xaa,-Asn-Xaa,-Xaa,-Xaa,-Asp-Arg-Cys-
Ser-Xaa,-Val-Arg (SEQ ID NO:179);

Gly-Gly-Cys-Cys-Ser-His-Xaa,-Val-Cys-Xaa,-Phe-Asn-Asn-Xaa,-Gln-Met-Cys-Arg
(SEQ ID NO:180);

Gly-Gly-Cys-Cys-Ser-His-Xaa,-Val-Cys-Asn-Leu-Asn-Asn-Xaa,-Gln-Met-Cys-Arg
(SEQ ID NO:181);

Gly-Cys-Cys-Ser-His-Xaa,-Xaa,-Cys-Xaa,-Ala-Asn-Asn-Gln-Ala-Xaa,-Cys-Asn
(SEQ ID NO:182);

Gly-Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ser-Val-Thr-His-Xaa,-Xaa,-Leu-Cys (SEQ
ID NO:183);

Gly-Gly-Cys-Cys-Ser-Xaa,-Xaa,-Ala-Cys-Ser-Val-Xaa,-His-Gln-Asp-Leu-Cys-Asp
(SEQ ID NO:184);

Val-Ser-Cys-Cys-Val-Val-Arg-Xaa,-Cys-Xaa,-Ile-Arg-Xaa,-Gln-Xaa,-Xaa,-Cys-
Leu-Xaa,-Ala-Asp-Xaa,-Arg-Thr-Leu (SEQ ID NO:185);

Xaa,-Asn-Cys-Cys-Ser-Ile-Xaa,-Gly-Cys-Xaa,-Xaa,-Xaa,-Xaa,-Gly-Asp-Xaa,-Cys-
Ser-Xaa,-Val-Arg (SEQ ID NO:186);

Gly-Cys-Cys-Ser-Asn-Xaa,-Val-Cys-His-Leu-Xaa,-His-Xaa,-Asn-Ala-Cys (SEQ
ID NO:187);

Gly-Cys-Cys-Ser-Asn-Xaa,-Ile-Cys-Xaa,-Phe-Asn-Asn-Xaa,-Arg-Ile-Cys-Arg (SEQ
ID NO:188);

Xaa,-Cys-Cys-Ser-Gln-Xaa,-Xaa,-Cys-Arg-Xaa,-Xaa,-His-Xaa,-Xaa,-Leu-Cys-Ser
(SEQ ID NO:189);

Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Ala-Gly-Asn-Asn-Gln-His-Ile-Cys (SEQ ID
NO:190);

Gly-Cys-Cys-Ala-Val-Xaa,-Ser-Cys-Arg-Leu-Arg-Asn-Xaa,-Asp-Leu-Cys-Gly-Gly
(SEQ ID NO:191);

Gly-Cys-Cys-Ser-His-Xaa,-Ala-Cys-Asn-Val-Asn-Asn-Xaa,-His-Ile-Cys (SEQ ID
NO:192);

Thr-Xaa,-Xaa,-Xaa,-Cys-Cys-Xaa,-Asn-Xaa,-Xaa,-Cys-Phe-Ala-Thr-Asn-Ser-Asp-
Ile-Cys-Gly (SEQ ID NO:193);

Asp-Ala-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ser-Gly-Xaa₂-His-Gln-Asp-Leu-Cys(SEQ ID NO:194);

Xaa₁-Asp-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Leu-Cys(SEQ ID NO:195);

5 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Ser-Asn-Ala-His-Ile-Cys (SEQ ID NO:196);

Xaa₁-Asp-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys (SEQ ID NO:197);

10 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Asn-Asn-Xaa₄-His-Ile-Cys (SEQ ID NO:198);

Gly-Cys-Cys-Gly-Asn-Xaa₅-Ser-Cys-Ser-Ile-His-Ile-Xaa₅-Xaa₄-Val-Cys-Asn (SEQ ID NO:199);

15 Thr-Asp-Ser-Xaa₁-Xaa₁-Cys-Cys-Leu-Asp-Ser-Arg-Cys-Ala-Gly-Gln-His-Gln-Asp-Leu-Cys-Gly (SEQ ID NO:200);

Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₄-Cys-Xaa₄-Ala-Asn-Asn-Gln-Ala-Xaa₄-Cys-Asn (SEQ ID NO:201);

20 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Val-Asn-Asn-Xaa₅-Asp-Ile-Cys (SEQ ID NO:202);

Gly-Xaa₂-Cys-Cys-Ile-Asn-Asp-Ala-Cys-Arg-Ser-Xaa₂-His-Xaa₅-Gln-Xaa₄-Cys-Ser (SEQ ID NO:203);

25 Gly-Cys-Cys-Xaa₄-Asn-Ile-Ala-Cys-Arg-Ile-Asn-Xaa₅-Arg-Xaa₄-Cys-Arg(SEQ ID NO:204);

Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Arg-Phe-Asn-Xaa₄-Xaa₅-Xaa₄-Cys-Gly (SEQ ID NO:205);

Asp-Xaa₁-Cys-Cys-Ala-Ser-Xaa₅-Xaa₄-Cys-Arg-Ile-Asn-Xaa₅-Xaa₄-Val-Cys-His (SEQ ID NO:206);

30 Gly-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-Xaa₅-Gln-Asn-Asn-Ala-Xaa₅-Xaa₄-Cys-Arg-Xaa₁-Ser (SEQ ID NO:207);

Gly-Cys-Cys-Ser-His-Xaa₅-Xaa₄-Cys-Ala-Gln-Asn-Asn-Gln-Asp-Xaa₄-Cys (SEQ ID NO:208);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ser-Gly-Asn-Asn-Arg-Xaa₅-Xaa₄-Cys-Arg-Xaa₁-Ser (SEQ ID NO:209);

Asp-Xaa₅-Cys-Cys-Ser-Xaa₄-Xaa₅-Asp-Cys-Gly-Ala-Asn-His-Xaa₅-Xaa₁-Ile-Cys-Gly (SEQ ID NO:210);

Xaa₁-Cys-Cys-Ser-Gln-Xaa₅-Xaa₅-Cys-Arg-Xaa₂-Xaa₂-His-Xaa₅-Xaa₁-Leu-Cys-Ser (SEQ ID NO:211);

5 Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Ala-Gly-Asn-Asn-Xaa₅-His-Ile-Cys (SEQ ID NO:212);

Gly-Cys-Cys-Ser-Asp-Xaa₅-Ser-Cys-Asn-Val-Asn-Asn-Xaa₅-Asp-Xaa₄-Cys (SEQ ID NO:213);

10 Xaa₁-Xaa₁-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys-Arg (SEQ ID NO:214);

Gly-Gly-Cys-Cys-Ser-Asn-Xaa₅-Ala-Cys-Leu-Val-Asn-His-Leu-Xaa₁-Met-Cys (SEQ ID NO:215);

15 Arg-Asp-Xaa₅-Cys-Cys-Phe-Asn-Xaa₅-Ala-Cys-Asn-Val-Asn-Asn-Xaa₅-Gln-Ile-Cys (SEQ ID NO:216);

Cys-Cys-Ser-Asp-Xaa₅-Ser-Cys-Xaa₅-Arg-Leu-His-Ser-Leu-Ala-Cys-Thr-Gly-Ile-Val-Asn-Arg (SEQ ID NO:217);

20 Cys-Cys-Thr-Asn-Xaa₅-Ala-Cys-Leu-Val-Asn-Asn-Ile-Arg-Phe-Cys-Gly (SEQ ID NO:218);

Asp-Xaa₁-Cys-Cys-Ser-Asp-Xaa₅-Arg-Cys-His-Gly-Asn-Asn-Arg-Asp-His-Cys-Ala (SEQ ID NO:219);

25 Asp-Cys-Cys-Ser-His-Xaa₅-Leu-Cys-Arg-Leu-Phe-Val-Xaa₅-Gly-Leu-Cys-Ile(SEQ ID NO:220);

Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Xaa₂-Val-Arg-Xaa₄-Xaa₅-Asp-Leu-Cys-Arg (SEQ ID NO:221);

Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asn-Asn-Xaa₅-His-Ile-Cys (SEQ ID NO:222);

30 Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Xaa₂-Val-Arg-Xaa₄-Ser-Asp-Met-Cys(SEQID NO:223);

Gly-Gly-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Xaa₂-Val-His-Phe-Xaa₅-His-Ser-Cys(SEQ ID NO:224);

Val-Cys-Cys-Ser-Asn-Xaa₅-Val-Cys-His-Val-Asp-His-Xaa₅-Xaa₁-Leu-Cys-Arg-Arg-Arg-Arg (SEQ ID NO:225);

Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Asn-Leu-Ser-Asn-Xaa₅-Gln-Ile-Cys-Arg (SEQ ID NO:226);

Xaa₆-Xaa₁-Cys-Cys-Ser-His-Xaa₅-Ala-Cys-Asn-Val-Asp-His-Xaa₅-Xaa₁-Ile-Cys-Arg (SEQ ID NO:227);

5 Gly-Cys-Cys-Ser-Asn-Xaa₅-Ala-Cys-Leu-Val-Asn-His-Ile-Arg-Phe-Cys-Gly (SEQ ID NO:228);

Asp-Cys-Cys-Asp-Asp-Xaa₅-Ala-Cys-Thr-Val-Asn-Asn-Xaa₅-Gly-Leu-Cys-Thr (SEQ ID NO:229); and

10 Gly-Cys-Cys-Ser-Asn-Xaa₅-Xaa₁-Cys-Ile-Ala-Xaa₂-Asn-Xaa₅-His-Met-Cys-Gly-Gly-Arg-Arg (SEQ ID NO:230),

wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₃ is Trp (D or L), halo-Trp or neo-Trp; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; Xaa₆ is Gln or pyro-Glu; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

22. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₂ is Lys.
23. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₁ is Glu.
24. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₃ is Trp.
25. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₄ is Tyr.
- 20 26. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₄ is mono-iodo-Tyr.
27. The substantially pure α -conotoxin peptide of claim 21, wherein Xaa₄ is di-iodo-Tyr.
28. The substantially pure α -conotoxin peptide of claim 20, which is modified to contain an O-glycan, an S-glycan or an N-glycan.

- 29 The substantially pure α -conotoxin peptide of claim 21 which is modified to contain an O-glycan, an S-glycan or an N-glycan.
30. A substantially pure α -conotoxin peptide selected from the group consisting of:
Cys-Cys-Thr-Ile-Xaa₅-Ser-Cys-Xaa₄-Xaa₁-Xaa₂-Xaa₂-Ile-Xaa₂-Ala-Cys-Val-
5 Phe (SEQ ID NO:231) and
Gly-Cys-Cys-Gly-Asn-Xaa₅-Ala-Cys-Ser-Gly-Ser-Ser-Xaa₂-Asp-Ala-Xaa₅-Ser-Cys
(SEQ ID NO:232),
wherein Xaa₁ is Glu or γ -carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys
10 or N,N,N-trimethyl-Lys; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and the C-terminus contains
a carboxyl or amide group, or derivatives thereof.
31. The substantially pure α -conotoxin peptide of claim 30, wherein Xaa₂ is Lys.
32. The substantially pure α -conotoxin peptide of claim 30, wherein Xaa₁ is Glu.
33. The substantially pure α -conotoxin peptide of claim 30, wherein Xaa₄ is Tyr.
- 15 34. The substantially pure α -conotoxin peptide of claim 30, wherein Xaa₄ is mono-iodo-Tyr.
35. The substantially pure α -conotoxin peptide of claim 30, wherein Xaa₄ is di-iodo-Tyr.
36. The substantially pure α -conotoxin peptide of claim 30, which is modified to contain an O-glycan, an S-glycan or an N-glycan.
- 20 37. An isolated nucleic acid comprising a nucleic acid coding for an α -conotoxin precursor
comprising an amino acid sequence selected from the group of amino acid sequences set
forth in Tables 1-134.

38. The nucleic acid of claim 37 wherein the nucleic acid comprises a nucleotide sequence selected from the group of nucleotide sequences set forth in Tables 1-134 or their complements.
39. A substantially pure α -conotoxin protein precursor comprising an amino acid sequence selected from the group of amino acid sequences set forth in Tables 1-134.
5

SEQUENCE LISTING

<110> University of Utah Research Foundation
Cogentix, Inc.

<120> Alpha-Conotoxin Peptides

<130> Alphas 2

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<150> US 60/118,381

<151> 1999-01-29

<160> 404

<170> PatentIn Ver. 2.0

<210> 1

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Alpha-Conotoxin Peptide Generic Formula I

<220>

<221> PEPTIDE

<222> (1)..(3)

<223> Xaa at residue 1 is des-Xaa, Ile, Leu or Val; Xaa at residue 2 is des-Xaa, Ala or Gly; Xaa at residue 3 is des-Xaa, Gly, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid.

<220>

<221> PEPTIDE

<222> (4)..(5)

<223> Xaa at residue 4 is des-Xaa, Gly, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa at residue 5 is Glu, gamma-carboxy-Glu (Gla), Asp, Ala, Thr, Ser, Gly, Ile, Tyr, nor-Tyr,

<220>

<221> PEPTIDE

<222> (5)..(8)

<223> mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa at residue 8 is Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys,

<220>

<221> PEPTIDE

<222> (8)..(9)

<223> N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa at residue 9 is Asp, Glu, Gla, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or

<220>
<221> PEPTIDE
<222> (9)..(11)
<223> any unnatural basic amino acid; Xaa at residue 10
is Ser, Thr, Asn, Ala, Gly, His, halo-His, Pro or
hydroxy-Pro; Xaa at residue 11 is Thr, Ser, Ala,
Asp, Asn, Pro, hydroxy-Pro,

<220>
<221> PEPTIDE
<222> (11)..(13)
<223> Arg, ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid; Xaa at residue 13 is
Gly, Ser, Thr, Ala, Asn,

<220>
<221> PEPTIDE
<222> (13)..(14)
<223> Arg, ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid; Xaa at residue 14 is
Gln, Leu, His, halo-His, Trp (D or L), halo-Trp,
neo-Trp,

<220>
<221> PEPTIDE
<222> (14)
<223> Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, Arg,
ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino

<220>
<221> PEPTIDE
<222> (14)..(15)
<223> acid or any unnatural aromatic amino acid; Xaa at
residue 15 is Asn, His, halo-His, Ile, Leu, Val,
Gln, Arg, ornithine, homoarginine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any

<220>
<221> PEPTIDE
<222> (15)..(16)
<223> unnatural basic amino acid; Xaa at residue 16 is
des-Xaa, Val, Ile, Leu, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid.

<400> 1
Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
1 5 10 15

Xaa

<210> 2
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Alpha-Conotoxin Peptide Generic Formula II.

<220>
<221> PEPTIDE
<222> (1)..(3)
<223> Xaa at residue 1 is des-Xaa, Asp, Glu or gamma-carboxy-Glu (Gla); Xaa at residue 2 is des-Xaa, Gln, Ala, Asp, Glu, Gla; Xaa at residue 3 is des-Xaa, Gly, Ala, Asp, Glu, Gla, Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (4)..(7)
<223> Xaa at residue 4 is des-Xaa4, Gly, Glu, Gla, Gln, Asp, Asn, Pro or hydroxy-Pro; Xaa at residue 7 is Ser, Thr, Gly, Glu, Gla, Asn, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine,

<220>
<221> PEPTIDE
<222> (7)
<223> Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy

<220>
<221> PEPTIDE
<222> (7)..(8)
<223> containing amino acid; Xaa at residue 8 is Asp, Asn, His, halo-His, Thr, Ser, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy

<220>
<221> PEPTIDE
<222> (8)..(10)
<223> containing amino acid; Xaa at residue 9 is Pro or hydroxy-Pro; Xaa at residue 10 is Ala, Ser, Thr, Asp, Val, Ile, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,

<220>
<221> PEPTIDE
<222> (10)..(12)
<223> O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa at residue 12 is Gly, Ile, Leu, Val, Ala, Thr, Ser, Pro, hydroxy-Pro, Phe, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine,

<220>
<221> PEPTIDE
<222> (12)..(13)
<223> homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa at residue 13 is Ala, Asn, Phe, Pro, hydroxy-Pro,

<220>

<221> PEPTIDE
<222> (13)
<223> Glu, Gln, Gln, His, halo-His, Val, Ser, Thr, Arg,
ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid.

<220>
<221> PEPTIDE
<222> (14)
<223> Xaa at residue 14 is Thr, Ser, His, halo-His, Leu,
Ile, Val, Asn, Met, Pro, hydroxy-Pro, Arg,
ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic

<220>
<221> PEPTIDE
<222> (14)..(15)
<223> amino acid, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr or any unnatural hydroxy containing
amino acid; Xaa at residue 15 is Asn, Pro,
hydroxy-Pro, Gln, Ser, Thr,

<220>
<221> PEPTIDE
<222> (15)
<223> Arg, ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys N,N,N-trimethyl-Lys, any
unnatural basic amino acid, Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr, nitro-Tyr

<220>
<221> PEPTIDE
<222> (15)..(16)
<223> or any unnatural hydroxy containing amino acid;
Xaa at residue 16 is des-Xaa, Gly, Thr, Ser, Pro,
hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr or any

<220>
<221> PEPTIDE
<222> (16)..(17)
<223> unnatural hydroxy containing amino acid; Xaa at
residue 17 is des-Xaa14, Ile, Val, Asp, Leu, Phe,
Arg, ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural

<220>
<221> PEPTIDE
<222> (17)..(19)
<223> basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr or any unnatural hydroxy containing
amino acid; Xaa at residue 19 is des-Xaa, Gly,
Ala, Met, Ser,

<220>
<221> PEPTIDE
<222> (19)

<223> Thr, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid.

<220>

<221> PEPTIDE

<222> (20)

<223> Xaa at residue 20 is des-Xaa, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any

<220>

<221> PEPTIDE

<222> (20)..(21)

<223> unnatural basic amino acid; Xaa at residue 21 is des-Xaa, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid.

<400> 2

Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Cys Xaa Xaa Xaa
20

<210> 3

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Alpha-Conotoxin Peptide Generic Formula III.

<220>

<221> PEPTIDE

<222> (1)..(3)

<223> Xaa at residue 1 is des-Xaa, Ser or Thr; Xaa at residue 2 is des-Xaa, Asp, Glu, -carboxy-Glu (Gla), Asn, Ser or Thr; Xaa at residue 3 is des-Xaa, Ala, Gly, Asn, Ser, Thr, Pro, hydroxy-Pro, Arg,

<220>

<221> PEPTIDE

<222> (3)..(4)

<223> ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa at residue 4 is des-Xaa, Ala, Val, Leu, Ile, Gly, Glu, Gla, Gln, Asp, Asn, Phe,

<220>

<221> PEPTIDE

<222> (4)..(5)

<223> Pro, hydroxy-Pro or any unnatural aromatic amino acid; Xaa at residue 5 is des-Xaa, Thr, Ser, Asp,

Glu, Gla, Gln, Gly, Val, Asp, Asn, Ala, Pro,
hydroxy-Pro, Arg, ornithine, homoarginine, Lys,

<220>
<221> PEPTIDE
<222> (5)..(8)
<223> N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid; Xaa at residue 8 is Thr, Ser, Asp, Asn, Met,
Val, Ala, Gly, Leu, Ile, Phe, any unnatural
aromatic amino acid,

<220>
<221> PEPTIDE
<222> (8)..(9)
<223> Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr or any unnatural hydroxy containing
amino acid; Xaa at residue 9 is Ile, Leu, Val,
Ser, Thr, Gln,

<220>
<221> PEPTIDE
<222> (9)
<223> Asn, Asp, Arg, His, halo-His, Phe, any unnatural
aromatic amino acid, homoarginine, ornithine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys, any unnatural basic amino
acid, Tyr, nor-Tyr,

<220>
<221> PEPTIDE
<222> (9)..(10)
<223> mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy
containing amino acid; Xaa at residue 10 is Pro,
hydroxy-Pro, Ser, Thr, Ile, Asp, Leu, Val, Gly,
Ala, Phe,

<220>
<221> PEPTIDE
<222> (10)..(11)
<223> any unnatural aromatic amino acid, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid; Xaa at residue 11 is Val, Ala, Gly, Ile,

<220>
<221> PEPTIDE
<222> (11)..(13)
<223> Leu, Asp, Ser, Thr, Pro, hydroxy-Pro, Arg,
ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid; Xaa at residue 13 is
His, halo-His,

<220>
<221> PEPTIDE
<222> (13)
<223> Arg, homoarginine, ornithine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino acid, Asn, Ala, Ser, Thr,
Phe, Ile, Leu, Gly, Trp (D or L), neo-Trp,
halo-Trp, any

<220>
<221> PEPTIDE
<222> (13)..(14)
<223> unnatural aromatic amino acid, Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy
containing amino acid; Xaa at residue 14 is Leu,
Gln, Val, Ile,

<220>
<221> PEPTIDE
<222> (14)
<223> Gly, Met, Ala, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Ser, Thr,
Arg, homoarginine, ornithine, any unnatural basic
amino acid, Asn, Glu, Gla, Gln, Phe, Trp (D or L),
neo-Trp,

<220>
<221> PEPTIDE
<222> (14)..(15)
<223> halo-Trp or any unnatural aromatic amino acid; Xaa
at residue 15 is Glu, Gla, Gln, Asn, Asp, Pro,
hydroxy-Pro, Ser, Gly, Thr, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Arg,

<220>
<221> PEPTIDE
<222> (15)
<223> homoarginine, ornithine, any unnatural basic amino
acid, Phe, His, halo-His, any unnatural aromatic
amino acid, Leu, Met, Gly, Ala, Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,

<220>
<221> PEPTIDE
<222> (15)..(16)
<223> O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy
containing amino acid; Xaa at residue 16 is His,
halo-His, Asn, Thr, Ser, Ile, Val, Leu, Phe, any
unnatural aromatic amino acid, Arg, homoarginine,

<220>
<221> PEPTIDE
<222> (16)
<223> ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys, any unnatural basic amino
acid, Tyr, nor-Try, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any
unnatural

<220>
<221> PEPTIDE
<222> (16)..(17)
<223> hydroxy containing amino acid; Xaa at residue 17
is Ser, Thr, Ala, Gln, Pro, hydroxy-Pro, Gly, Ile,
Leu, Arg, ornithine, homoarginine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any

<220>
<221> PEPTIDE
<222> (17)..(18)
<223> unnatural basic amino acid; Xaa at residue 18 is

Asn, Glu, Gla, Asp, Gly, His, halo-His, Ala, Leu,
Gln, Arg, ornithine, homoarginine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys, any

<220>
<221> PEPTIDE
<222> (18)..(19)
<223> unnatural basic amino acid, Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy
containing amino acid; Xaa at residue 19 is Met,
Ile, Thr, Ser,

<220>
<221> PEPTIDE
<222> (19)
<223> Val, Leu, Pro, hydroxy-Pro, Phe, any unnatural
aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
nitro-Tyr, any unnatural hydroxy containing amino
acid,

<220>
<221> PEPTIDE
<222> (19)..(21)
<223> Glu, Gla, Ala, His, halo-His, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid; Xaa at residue 21 is des-Xaa, Gly, Asp, Asn,

<220>
<221> PEPTIDE
<222> (21)..(22)
<223> Ala, Ile, Leu, Ser, Thr, His, halo-His, Arg,
ornithine, homoarginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
unnatural basic amino acid; Xaa at residue 22 is
des-Xaa, Gly,

<220>
<221> PEPTIDE
<222> (22)
<223> Glu, Gla, Gln, Trp (D or L), neo, halo-Trp, any
unnatural aromatic amino acid, Arg, ornithine,
homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid.

<220>
<221> PEPTIDE
<222> (23)
<223> Xaa at residue 23 is des-Xaa, Ser, Thr, Val, Ile,
Ala, Arg, ornithine, homoarginine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or any unnatural basic amino
acid.

<220>
<221> PEPTIDE
<222> (24)
<223> Xaa at residue 24 is des-Xaa, Val, Asp, His,
halo-His, Arg, ornithine, homoarginine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys,

N,N,N-trimethyl-Lys or any unnatural basic amino acid.

<220>
<221> PEPTIDE
<222> (25)...(26)
<223> Xaa at residue 25 is des-Xaa, Asn, Pro or hydroxy-Pro; Xaa at residue 26 is des-Xaa, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino

<220>
<221> PEPTIDE
<222> (26)...(28)
<223> acid; Xaa at residue 27 is des-Xaa, Ser or Thr; Xaa at residue 28 is des-Xaa, Leu, Ile or Val.

<400> 3
Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

<210> 4
<211> 14
<212> PRT
<213> Conus imperialis

<220>
<221> PEPTIDE
<222> (2)...(11)
<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residue 11 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 4
Asp Xaa Cys Cys Ser Asp Ser Arg Cys Gly Xaa Asn Cys Leu
1 5 10

<210> 5
<211> 12
<212> PRT
<213> Conus imperialis

<220>
<221> PEPTIDE
<222> (10)
<223> Xaa at residue 10 is Trp (D or L) or halo-Trp.

<400> 5
Ala Cys Cys Ser Asp Arg Arg Cys Arg Xaa Arg Cys
1 5 10

<210> 6
<211> 13
<212> PRT
<213> Conus regius

<400> 6

10

Phe Thr Cys Cys Arg Arg Gly Thr Cys Ser Gln His Cys
1 5 10

<210> 7
<211> 13
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (2)
<223> Xaa at residue 2 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 7
Asp Xaa Cys Cys Arg Arg His Ala Cys Thr Leu Ile Cys
1 5 10

<210> 8
<211> 13
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (2)..(8)
<223> Xaa at residue 2 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr; Xaa at residues 7 and 8 is Pro or
hydroxy-Pro.

<400> 8
Asp Xaa Cys Cys Arg Arg Xaa Xaa Cys Thr Leu Ile Cys
1 5 10

<210> 9
<211> 13
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(10)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at
residue 10 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 9
Gly Cys Cys Ser Asp Xaa Arg Cys Arg Xaa Arg Cys Arg
1 5 10

<210> 10
<211> 13
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE

II

<222> (7)..(11)
<223> Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 11 is Trp (D or L) or halo-Trp.

<400> 10
Gly Gly Cys Cys Ser Asp Xaa Arg Cys Ala Xaa Arg Cys
1 5 10

<210> 11
<211> 17
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (3)..(10)
<223> Xaa at residue 3 is Trp (D or L) or halo-Trp; Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa at residue 10 is Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (15)
<223> Xaa at residue 15 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 11
Ile Ala Xaa Asp Ile Cys Cys Ser Xaa Xaa Asp Cys Asn His Xaa Cys
1 5 10 15

Val

<210> 12
<211> 12
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(9)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 9 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 12
Gly Cys Cys Ser Asp Xaa Arg Cys Xaa His Gln Cys
1 5 10

<210> 13
<211> 14
<212> PRT
<213> Conus sponsalis

<220>
<221> PEPTIDE
<222> (5)..(11)
<223> Xaa at residues 5 and 11 is Pro or hydroxy-Pro; Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

12

<400> 13
Cys Cys Ser Asp Xaa Ala Cys Xaa Gln Thr Xaa Gly Cys Arg
1 5 10

<210> 14
<211> 13
<212> PRT
<213> Conus sponsalis

<220>
<221> PEPTIDE
<222> (3)..(5)
<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is Pro or hydroxy-Pro.

<400> 14
Cys Cys Xaa Asn Xaa Ala Cys Arg His Thr Gln Gly Cys
1 5 10

<210> 15
<211> 13
<212> PRT
<213> Conus sulcatus

<220>
<221> PEPTIDE
<222> (4)..(12)
<223> Xaa at residue 4 is Trp or halo-Trp; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 12 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 15
Gly Cys Cys Xaa His Xaa Ala Cys Gly Arg His Xaa Cys
1 5 10

<210> 16
<211> 14
<212> PRT
<213> Conus achatinus

<220>
<221> PEPTIDE
<222> (2)..(11)
<223> Xaa at residues 2 and 7 is Pro or hydroxy-Pro; Xaa at residue 11 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 16
Ala Xaa Cys Cys Asn Asn Xaa Ala Cys Val Xaa His Arg Cys
1 5 10

<210> 17
<211> 15
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (2)..(12)

<223> Xaa at residues 2 and 8 is Pro or hydroxy-Pro; Xaa at residue 12 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 17
Ala Xaa Gly Cys Cys Asn Asn Xaa Ala Cys Val Xaa His Arg Cys
1 5 10 15

<210> 18
<211> 14
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(11)
<223> Xaa at residues 1, 2 and 7 is Pro or hydroxy-Pro; Xaa at residue 11 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 18
Xaa Xaa Cys Cys Asn Asn Xaa Ala Cys Val Xaa His Arg Cys
1 5 10

<210> 19
<211> 16
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (2)..(13)
<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Trp or halo-Trp; Xaa at residues 8 11 and 13 is Pro or hydroxy-Pro.

<400> 19
Asp Xaa Asn Cys Cys Xaa Asn Xaa Ser Cys Xaa Arg Xaa Arg Cys Thr
1 5 10 15

<210> 20
<211> 13
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (6)..(12)
<223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residue 12 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 20
Gly Cys Cys Ser Arg Xaa Xaa Cys Ala Val Leu Xaa Cys
1 5 10

<210> 21
<211> 13
<212> PRT

<213> Conus circumcisus
<220>
<221> PEPTIDE
<222> (6)
<223> Xaa at residue 6 is Pro or hydroxy-Pro.

<400> 21
Gly Cys Cys Gly Asn Xaa Asp Cys Thr Ser His Ser Cys
1 5 10

<210> 22
<211> 16
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (6)..(11)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at
residue 11 is Glu or gamma-carboxy-Glu.

<400> 22
Gly Cys Cys Ser Asn Xaa Val Cys His Leu Xaa His Ser Asn Met Cys
1 5 10 15

<210> 23
<211> 17
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at
residue 14 is Glu or gamma-carboxy-Glu; Xaa at
residue 15 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 23
Gly Cys Cys Ser Asn Xaa Val Cys Arg Gln Asn Asn Ala Xaa Xaa Cys
1 5 10 15

Arg

<210> 24
<211> 18
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 24
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15

15

Cys Arg

<210> 25
<211> 18
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residues 2 and 15 is Glu or
gamma-carboxy-Glu.

<400> 25
Xaa Xaa Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15

Cys Arg

<210> 26
<211> 18
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 26
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15

Cys Asp

<210> 27
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 27
Xaa Arg Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15

Cys Arg

<210> 28
<211> 18

<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro.

<400> 28
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Gly Ile
1 5 10 15

Cys Arg

<210> 29
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 29
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Thr
1 5 10 15

Cys Arg

<210> 30
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 30
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Val
1 5 10 15

Cys Arg

<210> 31
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 31
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Ile Asp His Xaa Xaa Ile
1 5 10 15
Cys Arg

<210> 32
<211> 21
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)...(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 32
Xaa Gln Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15
Cys Arg Arg Arg Arg
20

<210> 33
<211> 17
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (7)...(15)
<223> Xaa at residues 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 33
Gly Gly Cys Cys Ser His Xaa Ala Cys Ala Val Asn His Xaa Xaa Leu
1 5 10 15

Cys

<210> 34
<211> 16
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (6)...(14)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<400> 34
Gly Cys Cys Ser His Xaa Ala Cys Ser Val Asn His Xaa Xaa Leu Cys
1 5 10 15

<210> 35
<211> 16

<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<400> 35
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile Cys
1 5 10 15

<210> 36
<211> 19
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (6)..(18)
<223> Xaa at residues 6 and 15 is Pro or hydroxy-Pro;
Xaa at residue 11 is Lys, N,-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at
residues 14 and 18 is Glu or gamma-carboxy-Glu.

<400> 36
Gly Cys Cys Ser His Xaa Ala Cys Ser Gly Xaa Thr Gln Xaa Xaa Cys
1 5 10 15

Arg Xaa Ser

<210> 37
<211> 18
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residues 1, 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<400> 37
Xaa Cys Cys Ser His Xaa Ala Cys Ser Gly Asn Asn Xaa Xaa Phe Cys
1 5 10 15

Arg Gln

<210> 38
<211> 18
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<400> 38
Gly Cys Cys Ser His Xaa Ala Cys Ser Gly Asn Asn Xaa Xaa Phe Cys
1 5 10 15

Arg Gln

<210> 39
<211> 16
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro;
Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 39
Gly Cys Cys Ser His Xaa Xaa Cys Ala Met Asn Asn Xaa Asp Xaa Cys
1 5 10 15

<210> 40
<211> 16
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residue 6, 7 and 13 is Pro or hydroxy-Pro;
Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 40
Gly Cys Cys Ser His Xaa Xaa Cys Phe Leu Asn Asn Xaa Asp Xaa Cys
1 5 10 15

<210> 41
<211> 17
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro;
Xaa at residue 11 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 41
Gly Cys Cys Ser Asn Xaa Xaa Cys Ile Ala Xaa Asn Xaa His Met Cys
1 5 10 15

Gly

20

<210> 42
<211> 16
<212> PRT
<213> Conus distans

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro.

<400> 42
Gly Cys Cys Ser Asn Xaa Xaa Cys Ala His Asn Asn Xaa Asp Cys Arg
1 5 10 15

<210> 43
<211> 17
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 43
Gly Cys Cys Ser Asn Xaa Ala Cys Ala Gly Asn Asn Xaa His Val Cys
1 5 10 15

Arg

<210> 44
<211> 16
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 44
Gly Cys Cys Ser Arg Xaa Ala Cys Ile Ala Asn Asn Xaa Asp Leu Cys
1 5 10 15

<210> 45
<211> 20
<212> PRT
<213> Conus circumcisus

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residues 11 and 14 is Glu or
gamma-carboxy-Glu.

<400> 45
Gly Cys Cys Ser Asn Xaa Val Cys His Val Xaa His Xaa Xaa Leu Cys
1 5 10 15

Arg Arg Arg Arg
20

<210> 46
<211> 18
<212> PRT
<213> Conus sulcatus

<220>
<221> PEPTIDE
<222> (7)..(15)
<223> Xaa at residues 7, 12 and 14 is Pro or
hydroxy-Pro; Xaa at residue 11 is Lys,
N-methyl-Lys, N,N-dimethyl-Lys or
N,N,N-trimethyl-Lys; Xaa at residue 15 is Glu or
gamma-carboxy-Glu.

<400> 46
Gly Gly Cys Cys Ser Phe Xaa Ala Cys Arg Xaa Xaa Arg Xaa Xaa Met
1 5 10 15

Cys Gly

<210> 47
<211> 18
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro;
Xaa at residues 2 and 15 is Glu or
gamma-carboxy-Glu.

<400> 47
Xaa Xaa Cys Cys Ser Asp Xaa Arg Cys Asn Ser Ser His Xaa Xaa Leu
1 5 10 15

Cys Arg

<210> 48
<211> 18
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 48
Xaa Gln Cys Cys Ser Asp Xaa Arg Cys Asn Val Gly His Xaa Xaa Leu
1 5 10 15

Cys Gly

<210> 49
<211> 18
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 7 and 14 is Pro or hydroxy-Pro; Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 49
Xaa Val Cys Cys Ser Asp Xaa Arg Cys Asn Val Gly His Xaa Xaa Ile
1 5 10 15

Cys Gly

<210> 50
<211> 16
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro.

<400> 50
Gly Cys Cys Ser Arg Xaa Xaa Cys Ile Ala Asn Asn Xaa Asp Leu Cys
1 5 10 15

<210> 51
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1 and 14 is Pro or hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 51
Xaa Gln Cys Cys Ser His Leu Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15

Cys Arg

<210> 52
<211> 19
<212> PRT
<213> Conus sulcatus

<220>
<221> PEPTIDE
<222> (5)..(14)
<223> Xaa at residue 5 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or

nitro-Tyr; Xaa at residue 13 is Pro or hydroxy-Pro; Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<220>
<221> PEPTIDE
<222> (18)
<223> Xaa at residue 18 is Trp or halo-Trp.

<400> 52
Gly Cys Cys Ser Xaa Phe Asp Cys Arg Met Met Phe Xaa Xaa Met Cys
1 5 10 15

Gly Xaa Arg

<210> 53
<211> 18
<212> PRT
<213> Conus sulcatus

<220>
<221> PEPTIDE
<222> (11)..(12)
<223> Xaa at residue 11 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at residue 12 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<220>
<221> PEPTIDE
<222> (14)..(15)
<223> Xaa at residue 14 is Pro or hydroxy-Pro; Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 53
Gly Gly Cys Cys Ser Phe Ala Ala Cys Arg Xaa Xaa Arg Xaa Xaa Met
1 5 10 15

Cys Gly

<210> 54
<211> 20
<212> PRT
<213> Conus sulcatus

<220>
<221> PEPTIDE
<222> (7)..(15)
<223> Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 54
Gly Gly Cys Cys Phe His Xaa Val Cys Xaa Ile Asn Leu Leu Xaa Met
1 5 10 15

Cys Arg Gln Arg

<210> 55
<211> 19
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (7)..(15)
<223> Xaa at residues 7, 11 and 14 is Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr; Xaa at residues 8, 9 and 15 is Pro
or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (12)..(16)
<223> Xaa at residues 12 and 16 is Glu or
gamma-carboxy-Glu.

<400> 55
Ser Ala Thr Cys Cys Asn Xaa Xaa Xaa Cys Xaa Xaa Thr Xaa Xaa Xaa
1 5 10 15

Ser Cys Leu

<210> 56
<211> 17
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (5)..(13)
<223> Xaa at residues 5 and 12 is Tyr, no-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr or nitro-Tyr; Xaa at residues 6, 7
and 13 is Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (10)..(14)
<223> Xaa at residues 10 and 14 is Glu or
gamma-carboxy-Glu.

<400> 56
Ala Cys Cys Ala Xaa Xaa Xaa Cys Phe Xaa Ala Xaa Xaa Xaa Arg Cys
1 5 10 15

Leu

<210> 57
<211> 19
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE

<222> (3)..(16)
<223> Xaa at residues 3, 12 and 16 is Glu or
gamma-carboxy-Glu; Xaa at residues 6, 7, 11 and 14
is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<220>
<221> PEPTIDE
<222> (8)..(15)
<223> Xaa at residues 8, 9 and 15 is Pro or hydroxy-Pro.

<400> 57
Asn Ala Xaa Cys Cys Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Xaa Xaa
1 5 10 15

Ile Cys Leu

<210> 58
<211> 227
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(189)

<400> 58
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac 96
Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp
20 25 30

aaa gcg tct gac gtg atc acg ctg gcc ctc aag gga tgc tgt tcc aac 144
Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn
35 40 45

cct gtc tgt cac ttg gag cat tca aac ctt tgt ggt aga aga cgc 189
Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg
50 55 60

tgatgctcca ggaccctctg aaccacgacg ttcgagca 227

<210> 59
<211> 63
<212> PRT
<213> Conus magus

<400> 59
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp
20 25 30

Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn
35 40 45

Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg

50

55

60

<210> 60
<211> 208
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (1)..(168)

<400> 60
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca gat cgt gca tct gat ggc agg aag gac gca gcg tct ggc 96
Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly
20 25 30

ctg atc gct ctg acc atc aag gga tgc tgt tct tat cct ccc tgt ttc 144
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe
35 40 45

gcg act aat tca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga 198
Ala Thr Asn Ser Asp Tyr Cys Gly
50 55

accacgacgt 208

<210> 61
<211> 56
<212> PRT
<213> Conus aulicus

<400> 61
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly
20 25 30

Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe
35 40 45

Ala Thr Asn Ser Asp Tyr Cys Gly
50 55

<210> 62
<211> 205
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (1)..(174)

<400> 62
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca gat cgt gca tct gat ggc agg aag gac gca gcg tct ggc 96
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly
 20 25 30

ctg att gct ctg acc atg aag gga tgc tgt tat cct ccc tgt ttc 144
 Leu Ile Ala Leu Thr Met Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe
 35 40 45

gcg act aat cca gac tgt ggt cga cga cgc tgatgctcca ggaccctctg 194
 Ala Thr Asn Pro Asp Cys Gly Arg Arg Arg
 50 55

aaccacgacg t 205

<210> 63
<211> 58
<212> PRT
<213> Conus aulicus

<400> 63
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Lys Asp Ala Ala Ser Gly
 20 25 30

Leu Ile Ala Leu Thr Met Lys Gly Cys Cys Ser Tyr Pro Pro Cys Phe
 35 40 45

Ala Thr Asn Pro Asp Cys Gly Arg Arg Arg
 50 55

<210> 64
<211> 223
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)..(192)

<400> 64
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc tct tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa 96
Phe Ser Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Lys
 20 25 30

gcg tct ggc ctg gtc agt ctg act gac agg aga cca gaa tgc tgt agt 144
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
 35 40 45

gat cct cgc tgt aac tcg agt cat cca gaa ctt tgt ggt gga aga cgc 192
Asp Pro Arg Cys Asn Ser Ser His Pro Glu Leu Cys Gly Gly Arg Arg
 50 55 60

tgatgctcca ggaccctctg aaccacgacg t 223

<210> 65

<211> 64
<212> PRT
<213> Conus textile

<400> 65
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Ser Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Ala Lys
20 25 30

Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
35 40 45

Asp Pro Arg Cys Asn Ser Ser His Pro Glu Leu Cys Gly Gly Arg Arg
50 55 60

<210> 66
<211> 244
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)...(168)

<400> 66
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc gcc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Val Ser
1 5 10 15

ttc act tca gat cgt gca tct gat gac ggg aaa gcc gct gcg tct gac 96
Phe Thr Ser Asp Arg Ala Ser Asp Asp Gly Lys Ala Ala Ala Ser Asp
20 25 30

ctg atc act ctg acc atc aag gga tgc tgt tct cgt cct ccc tgt atc 144
Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile
35 40 45

gcg aat aat cca gac ttg tgt ggt tgacgacgct gatgctccag aacggctgta 198
Ala Asn Asn Pro Asp Leu Cys Gly
50 55

accacgacgt tcgagcaatg ttcaccgtgt ttctgttgt tgcatt 244

<210> 67
<211> 56
<212> PRT
<213> Conus textile

<400> 67
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Val Ser
1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Asp Gly Lys Ala Ala Ala Ser Asp
20 25 30

Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile
35 40 45

Ala Asn Asn Pro Asp Leu Cys Gly
50 55

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<210> 68
<211> 223
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)..(183)

<400> 68
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc      48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
    1           5           10          15

ttc act tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa      96
Phe Thr Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Lys
    20          25          30

gcg tct ggc ctg gtc agt ctg act gac agg aga cca caa tgc tgt tct      144
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser
    35          40          45

cat cct gcc tgt aac gta gat cat cca gaa att tgt cgt tgaagacgct      193
His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg
    50          55          60

gatgctccag gaccctctga accacgacgt                                223

<210> 69
<211> 61
<212> PRT
<213> Conus textile

<400> 69
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
    1           5           10          15

Phe Thr Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Lys
    20          25          30

Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser
    35          40          45

His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg
    50          55          60

<210> 70
<211> 223
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (1)..(183)

<400> 70
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc      48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
    1           5           10          15

ttc act tca ggt cgt cgt aca ttt cat ggc agg aat gcc gca gcc aaa      96

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30

Phe Thr Ser Gly Arg Arg Thr Phe His Gly Arg Asn Ala Ala Ala Lys
 20 25 30

gcg tct ggc ctg gtc agt ctg act gac agg aga cca gaa tgc tgt tct 144
 Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
 35 40 45

cat cct gcc tgt aac gta gat cat cca gaa att tgt cgt tgaagacgct 193
 His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg
 50 55 60

gatgctccag gaccctctga accacgacgt 223

<210> 71
<211> 61
<212> PRT
<213> Conus radiatus

<400> 71
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Gly Arg Arg Thr Phe His Gly Arg Asn Ala Ala Ala Lys
 20 25 30

Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
 35 40 45

His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Arg
 50 55 60

<210> 72
<211> 223
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (1)..(183)

<400> 72
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

tgc act tca ggt cgt agt aca ttt cgt ggc agg aat gcc gca gcc aaa 96
Phe Thr Ser Gly Arg Ser Thr Phe Arg Gly Arg Asn Ala Ala Lys
 20 25 30

gcg tct ggc ctg gtc agt ctg act gac agg aga cca caa tgc tgt tct 144
Ala Ser Gly Leu Val Ser Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser
 35 40 45

cat cct gcc tgt aac gta gat cat cca gaa att tgc gat tgaagacgct 193
His Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Asp
 50 55 60

gatgctccag gaccctctga accacgacgt 223

<210> 73
<211> 61

<212> PRT

<213> Conus radiatus

<400> 73

Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser
1				5					10				15		
Phe	Thr	Ser	Gly	Arg	Ser	Thr	Phe	Arg	Gly	Arg	Asn	Ala	Ala	Ala	Lys
	20					25					30				
Ala	Ser	Gly	Leu	Val	Ser	Leu	Thr	Asp	Arg	Arg	Pro	Gln	Cys	Cys	Ser
	35					40					45				
His	Pro	Ala	Cys	Asn	Val	Asp	His	Pro	Glu	Ile	Cys	Asp			
	50					55				60					

<210> 74

<211> 218

<212> DNA

<213> Conus striatus

<220>

<221> CDS

<222> (1)..(171)

<400> 74

atg	ttc	act	gtg	ttt	ctg	ttg	gtc	ttg	gca	atc	act	gtc	gtt	tcc	48
Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Ile	Thr	Val	Val	Ser
1					5				10				15		
tta	cct	tta	aat	cgf	gaa	tct	aat	ggc	gaa	aat	gcc	gaa	gcc	cgc	acc
Phe	Pro	Leu	Asp	Arg	Glu	Ser	Asp	Gly	Ala	Asn	Ala	Glu	Ala	Arg	Thr
	20						25					30			
cac	gat	cat	gag	aag	cac	gca	ctg	gac	cgg	aat	gga	tgc	tgt	agg	aat
His	Asp	His	Glu	Lys	His	Ala	Leu	Asp	Arg	Asn	Gly	Cys	Cys	Arg	Asn
	35						40				45				
cct	gcc	tgt	gag	agc	cac	aga	tgt	ggt	tgacgacgct	aat	gtatgtccag				144
Pro	Ala	Cys	Glu	Ser	His	Arg	Cys	Gly							191
	50						55								
gaccctctga	accacgacgt	tcgagca													218

<210> 75

<211> 57

<212> PRT

<213> Conus striatus

<400> 75

Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Ile	Thr	Val	Val	Ser
1					5				10				15		
Phe	Pro	Leu	Asp	Arg	Glu	Ser	Asp	Gly	Ala	Asn	Ala	Glu	Ala	Arg	Thr
	20						25					30			
His	Asp	His	Glu	Lys	His	Ala	Leu	Asp	Arg	Asn	Gly	Cys	Cys	Arg	Asn
	35						40				45				
Pro	Ala	Cys	Glu	Ser	His	Arg	Cys	Gly							
	50						55								

<210> 76
<211> 227
<212> DNA
<213> Conus bandanus

<220>
<221> CDS
<222> (1)..(180)

<400> 76
atg ttc acc atg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Met Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc gct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aag gac 96
Phe Ala Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Lys Asp
20 25 30

aaa gcg tct gac ctg gtc gct ctg acc gtc aag gga tgc tgt tct cat 144
Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys Ser His
35 40 45

cct gcc tgt agc gtg aat aat cca gac att tgt ggt tgaagacgt 190
Pro Ala Cys Ser Val Asn Asn Pro Asp Ile Cys Gly
50 55 60

gatgctccag gaccctctga accacgacgt tcgagaca 227

<210> 77
<211> 60
<212> PRT
<213> Conus bandanus

<400> 77
Met Phe Thr Met Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Ala Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Lys Asp
20 25 30

Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys Ser His
35 40 45

Pro Ala Cys Ser Val Asn Asn Pro Asp Ile Cys Gly
50 55 60

<210> 78
<211> 104
<212> DNA
<213> Conus bandanus

<220>
<221> CDS
<222> (1)..(54)

<400> 78
aaa gaa tgc tgt act cat cct gcc tgt cac gtg agt cat cca gaa ctc 48
Lys Glu Cys Cys Thr His Pro Ala Cys His Val Ser His Pro Glu Leu
1 5 10 15

tgt ggt tgaaaagcga cgtgacgctc caggaccctc tgaaccacga cgttcgagca 104
Cys Gly

<210> 79
<211> 18
<212> PRT
<213> Conus bandanus

<400> 79
Lys Glu Cys Cys Thr His Pro Ala Cys His Val Ser His Pro Glu Leu
1 5 10 15

Cys Gly

<210> 80
<211> 206
<212> DNA
<213> Conus bandanus

<220>
<221> CDS
<222> (1)...(171)

<400> 80
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act gct gtt ctt cca 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro
1 5 10 15

gtc act tta gat cgt gca tct gat gga agg aat gca gca gcc aac gcc 96
Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
20 25 30

aaa acg cct cgc ctg atc gcg cca ttc atc agg gat tat tgc tgt cat 144
Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His
35 40 45

aga ggt ccc tgt atg gta tgg tgt ggt tgaagccgct gctgctccag 191
Arg Gly Pro Cys Met Val Trp Cys Gly
50 55

gaccctctga accac 206

<210> 81
<211> 57
<212> PRT
<213> Conus bandanus

<400> 81
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro
1 5 10 15

Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
20 25 30

Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His
35 40 45

Arg Gly Pro Cys Met Val Trp Cys Gly
50 55

<210> 82
<211> 174

<212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)...(171)

<400> 82
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 ttc act tca gat cgt gct tct gat ggc agg aat gcc gca gcc aac gcg 96
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
 20 25 30
 ttt gac ctg atc gct ctg atc gcc agg caa aat tgc tgt agc att ccc 144
 Phe Asp Leu Ile Ala Leu Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro
 35 40 45
 agc tgt tgg gag aaa tat aaa tgt agt taa 174
 Ser Cys Trp Glu Lys Tyr Lys Cys Ser
 50 55

/
 <210> 83
 <211> 57
 <212> PRT
 <213> Conus characteristicus

<400> 83
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
 20 25 30
 Phe Asp Leu Ile Ala Leu Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro
 35 40 45
 Ser Cys Trp Glu Lys Tyr Lys Cys Ser
 50 55

<210> 84
 <211> 219
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)...(189)

<400> 84
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 ttc act tca gat cgt gct gaa ggc agg aat gct gca gcc aag gac 96
 Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Ala Lys Asp
 20 25 30
 aaa gcg tct gac ctg gtg gct ctg aca gtc agg gga tgc tgt gcc att 144
 Lys Ala Ser Asp Leu Val Ala Leu Thr Val Arg Gly Cys Cys Ala Ile

35

40

45

cgt gaa tgt cgc ttg cag aat gca gcg tat tgt ggt gga ata tac 189
 Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile Tyr
 50 55 60

tgatgctcca ggaccctctg aaccacgacg 219

<210> 85
<211> 63
<212> PRT
<213> Conus characteristicus

<400> 85
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Lys Asp
 20 25 30

Lys Ala Ser Asp Leu Val Ala Leu Thr Val Arg Gly Cys Cys Ala Ile
 35 40 45

Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile Tyr
 50 55 60

<210> 86
<211> 217
<212> DNA
<213> Conus tulipa

<220>
<221> CDS
<222> (1)..(186)

<400> 86
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc cct tca gat att gca act gag ggc agg aat gcc gca gcc aaa gcg 96
 Phe Pro Ser Asp Ile Ala Thr Glu Gly Arg Asn Ala Ala Lys Ala
 20 25 30

ttt gac ctg ata tct tcg atc gtc aag aaa gga tgc tgt tcc cat cct 144
 Phe Asp Leu Ile Ser Ser Ile Val Lys Lys Gly Cys Cys Ser His Pro
 35 40 45

gcc tgt tcg ggg aat aat cca gaa ttt tgt cgt caa ggt cgc 186
 Ala Cys Ser Gly Asn Asn Pro Glu Phe Cys Arg Gln Gly Arg
 50 55 60

tgatgctcca ggaccctctg aaccacgacg t 217

<210> 87
<211> 62
<212> PRT
<213> Conus tulipa

<400> 87
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

36

1	5	10	15												
Phe	Pro	Ser	Asp	Ile	Ala	Thr	Glu	Gly	Arg	Asn	Ala	Ala	Ala	Lys	Ala
				20			25						30		

Phe	Asp	Leu	Ile	Ser	Ser	Ile	Val	Lys	Lys	Gly	Cys	Cys	Ser	His	Pro
				35			40					45			

Ala	Cys	Ser	Gly	Asn	Asn	Pro	Glu	Phe	Cys	Arg	Gln	Gly	Arg		
				50			55				60				

<210> 88
<211> 217
<212> DNA
<213> Conus tulipa

<220>
<221> CDS
<222> (1)..(186)

1	5	10	15	48											
atg	tgc	acc	gtg	ttt	ctg	ttg	gtc	ttg	gca	acc	act	gtc	gtt	tcc	
Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser
20															
ttc	cct	tca	gat	ata	gca	act	gag	ggc	agg	aat	gcc	gca	gcc	aaa	gcg
Phe	Pro	Ser	Asp	Ile	Ala	Thr	Glu	Gly	Arg	Asn	Ala	Ala	Ala	Lys	Ala
				25			30								
ttt	gac	ctg	ata	tct	tgc	atc	gtc	agg	aaa	gga	tgc	tgt	tcc	aat	ccc
Phe	Asp	Leu	Ile	Ser	Ser	Ile	Val	Arg	Lys	Gly	Cys	Cys	Ser	Asn	Pro
				35			40				45				
gcc	tgt	gct	ggg	aat	aat	cca	cat	gtt	tgt	cgt	caa	ggg	cg		
Ala	Cys	Ala	Gly	Asn	Asn	Pro	His	Val	Cys	Arg	Gln	Gly	Arg		
				50			55				60				

tgatgctcca ggaccctctg aaccacgacg t 217

<210> 89
<211> 62
<212> PRT
<213> Conus tulipa

1	5	10	15												
Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser
20															
Phe	Pro	Ser	Asp	Ile	Ala	Thr	Glu	Gly	Arg	Asn	Ala	Ala	Ala	Lys	Ala
35															
Phe	Asp	Leu	Ile	Ser	Ser	Ile	Val	Arg	Lys	Gly	Cys	Cys	Ser	Asn	Pro
Ala	Cys	Ala	Gly	Asn	Asn	Pro	His	Val	Cys	Arg	Gln	Gly	Arg		
50															

<210> 90
<211> 226
<212> DNA
<213> Conus sulcatus

<220>
<221> CDS
<222> (1)..(195)

<400> 90
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc 96
Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala
20 25 30
aaa gcg tct gac aag atc gct tcg acc ctc aag aga aga gga tgc tgt 144
Lys Ala Ser Asp Lys Ile Ala Ser Thr Leu Lys Arg Arg Gly Cys Cys
35 40 45
tcg tat ttt gac tgt aga atg atg ttt cca gaa atg tgt ggt tgg cga 192
Ser Tyr Phe Asp Cys Arg Met Met Phe Pro Glu Met Cys Gly Trp Arg
50 55 60
ggc tgatgctcca ggaccctctg aaccacgacg t 226
Gly
65

<210> 91
<211> 65
<212> PRT
<213> Conus sulcatus

<400> 91
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala
20 25 30
Lys Ala Ser Asp Lys Ile Ala Ser Thr Leu Lys Arg Arg Gly Cys Cys
35 40 45
Ser Tyr Phe Asp Cys Arg Met Met Phe Pro Glu Met Cys Gly Trp Arg
50 55 60
Gly
65

<210> 92
<211> 226
<212> DNA
<213> Conus sulcatus

<220>
<221> CDS
<222> (1)..(195)

<400> 92
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc 96
Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala

20

25

30

ata gcg tct gac aag atc gct tcg acc ctc agg aga gga gga tgc tgt 144
 Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys
 35 40 45

tct ttt cct gcc tgt aga aag tat cgt cca gaa atg tgt ggt gga cga 192
 Ser Phe Pro Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg
 50 55 60

cgc tgatgctcca ggaccctctg aaccacgacg t 226
 Arg
 65

<210> 93

<211> 65

<212> PRT

<213> Conus sulcatus

<400> 93
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala
 20 25 30

Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys
 35 40 45

Ser Phe Pro Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg
 50 55 60

Arg
 65

<210> 94

<211> 211

<212> DNA

<213> Conus sulcatus

<220>
 <221> CDS
 <222> (1)...(180)

<400> 94

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc act tca gat cat gaa tct gat cgc ggt gat gcc caa acc atc caa 96
 Phe Thr Ser Asp His Glu Ser Asp Arg Gly Asp Ala Gln Thr Ile Gln
 20 25 30

gaa gtg ttt gag atg ttc gct ctg gac agc gat gga tgc tgt tgg cat 144
 Glu Val Phe Glu Met Phe Ala Leu Asp Ser Asp Gly Cys Cys Trp His
 35 40 45

cct gct tgt ggc aga cac tat tgt ggt cga aga cgc tgatgctcca 190
 Pro Ala Cys Gly Arg His Tyr Cys Gly Arg Arg Arg
 50 55 60

ggaccctctg aaccacgacg t 211

<210> 95
 <211> 60
 <212> PRT
 <213> Conus sulcatus

<400> 95
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp His Glu Ser Asp Arg Gly Asp Ala Gln Thr Ile Gln
 20 25 30

Glu Val Phe Glu Met Phe Ala Leu Asp Ser Asp Gly Cys Cys Trp His
 35 40 45

Pro Ala Cys Gly Arg His Tyr Cys Gly Arg Arg Arg
 50 55 60

<210> 96
 <211> 202
 <212> DNA
 <213> Conus sulcatus

<220>
 <221> CDS
 <222> (1)..(195)

<400> 96
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc aat tca gat cgt gat cca gca tta ggt ggc agg aat gct gca gcc 96
 Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala
 20 25 30

ata gcg tct gac aag atc gct tcg acc ctc agg aga gga gga tgc tgt 144
 Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys
 35 40 45

tct ttt gct gcc tgt aga aag tat cgt cca gaa atg tgt ggt gga cga 192
 Ser Phe Ala Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg
 50 55 60

cgc tgatgct 202
 Arg
 65

<210> 97
 <211> 65
 <212> PRT
 <213> Conus sulcatus

<400> 97
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Asn Ser Asp Arg Asp Pro Ala Leu Gly Gly Arg Asn Ala Ala Ala
 20 25 30

Ile Ala Ser Asp Lys Ile Ala Ser Thr Leu Arg Arg Gly Gly Cys Cys

40

35

40

45

Ser Phe Ala Ala Cys Arg Lys Tyr Arg Pro Glu Met Cys Gly Gly Arg
 50 55 60

Arg
 65

<210> 98
 <211> 220
 <212> DNA
 <213> Conus sulcatus

<220>
 <221> CDS
 <222> (1)..(189)

<400> 98
 atg ttc acc gtg ttt ctg ttg gtt ctc ttg gca acc acc gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc aat tca gat cgt gca tta ggt ggc agg aat gct gca gcc aaa gcg 96
 Phe Asn Ser Asp Arg Ala Leu Gly Arg Asn Ala Ala Lys Ala
 20 25 30

tct gac aag atc ctt tcg aac ctc agg aga gga gga tgc tgt ttt cat 144
 Ser Asp Lys Ile Leu Ser Asn Leu Arg Arg Gly Cys Cys Phe His
 35 40 45

cct gtc tgt tac atc aat ctt cta gaa atg tgt cgt caa cga ggc 189
 Pro Val Cys Tyr Ile Asn Leu Leu Glu Met Cys Arg Gln Arg Gly
 50 55 60

tgatcgcca ggaccctctg aaccacgacg t 220

<210> 99
 <211> 63
 <212> PRT
 <213> Conus sulcatus

<400> 99
 Met Phe Thr Val Phe Leu Leu Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Asn Ser Asp Arg Ala Leu Gly Arg Asn Ala Ala Lys Ala
 20 25 30

Ser Asp Lys Ile Leu Ser Asn Leu Arg Arg Gly Cys Cys Phe His
 35 40 45

Pro Val Cys Tyr Ile Asn Leu Leu Glu Met Cys Arg Gln Arg Gly
 50 55 60

<210> 100
 <211> 208
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS

<222> (1)..(177)

<400> 100
atg ttc acc gtg ttt ctg ttg gtc ttg aca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser
1 5 10 15

ttc cct tca gat agt gca tct gat gtc agg gat gac gaa gcc aaa gac 96
Phe Pro Ser Asp Ser Ala Ser Asp Val Arg Asp Asp Glu Ala Lys Asp
20 25 30

gaa agg tct gac atg tac aaa tcg aaa cg^g aat gga cgc tgt tgc cat 144
Glu Arg Ser Asp Met Tyr Lys Ser Lys Arg Asn Gly Arg Cys Cys His
35 40 45

cct gcc tgt ggc aaa cac ttt agt tgt gga cgc tgatgctcca ggaccctctg 197
Pro Ala Cys Gly Lys His Phe Ser Cys Gly Arg
50 55

aaccacgacg t 208

<210> 101
<211> 59
<212> PRT
<213> Conus consors

<400> 101
Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser
1 5 10 15

Phe Pro Ser Asp Ser Ala Ser Asp Val Arg Asp Asp Glu Ala Lys Asp
20 25 30

Glu Arg Ser Asp Met Tyr Lys Ser Lys Arg Asn Gly Arg Cys Cys His
35 40 45

Pro Ala Cys Gly Lys His Phe Ser Cys Gly Arg
50 55

<210> 102
<211> 219
<212> DNA
<213> Conus stercusmuscarum

<220>
<221> CDS
<222> (1)..(189)

<400> 102
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

tcc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gag 96
Ser Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Glu
20 25 30

aaa gcg tct gac gtg atc gcg ctg gcc ctc aag gga tgc tgt tcc aac 144
Lys Ala Ser Asp Val Ile Ala Leu Ala Leu Lys Gly Cys Cys Ser Asn
35 40 45

cct gtc tgt cac ctg gag cat tca aac atg tgt ggt aga aga cgc 189

42

Pro Val Cys His Leu Glu His Ser Asn Met Cys Gly Arg Arg Arg
 50 55 60

tgatgctcca ggaccctctg aaccacgacg 219

<210> 103
<211> 63
<212> PRT
<213> Conus stercusmuscarum

<400> 103
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ser Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Glu
 20 25 30

Lys Ala Ser Asp Val Ile Ala Leu Ala Leu Lys Gly Cys Cys Ser Asn
 35 40 45

Pro Val Cys His Leu Glu His Ser Asn Met Cys Gly Arg Arg Arg
 50 55 60

<210> 104
<211> 248
<212> DNA
<213> Conus betulinus

<220>
<221> CDS
<222> (1)...(180)

<400> 104
atg ttc tcc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Ser Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

tcc act tca ggt ggt gca tct ggt ggc agg aag gct gca gcc aaa gcg 96
Ser Thr Ser Gly Gly Ala Ser Gly Gly Arg Lys Ala Ala Ala Lys Ala
 20 25 30

tct aac cgg atc gct ctg acc gtc agg agt gca aca tgc tgt aat tat 144
Ser Asn Arg Ile Ala Leu Thr Val Arg Ser Ala Thr Cys Cys Asn Tyr
 35 40 45

cct ccc tgt tac gag act tat cca gaa agt tgt ctg taacgtgaat 190
Pro Pro Cys Tyr Glu Thr Tyr Pro Glu Ser Cys Leu
 50 55 60

catccagagc tttgtggctg aagacactga tgctccagga ccctctgaac cacgacgt 248

<210> 105
<211> 60
<212> PRT
<213> Conus betulinus

<400> 105
Met Phe Ser Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ser Thr Ser Gly Gly Ala Ser Gly Gly Arg Lys Ala Ala Ala Lys Ala

43

20	25	30
----	----	----

Ser Asn Arg Ile Ala Leu Thr Val Arg Ser Ala Thr Cys Cys Asn Tyr	40	45
35		

Pro Pro Cys Tyr Glu Thr Tyr Pro Glu Ser Cys Leu	55	60
50		

<210> 106
<211> 223
<212> DNA
<213> Conus betulinus

<220>
<221> CDS
<222> (1)...(183)

<400> 106
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca ggt cgt gca ttt cgt ggc agg aat cgc gca gcc gac gac	25	96
Phe Thr Ser Gly Arg Ala Phe Arg Gly Arg Asn Arg Ala Ala Asp Asp		
20	25	30

aaa agg tct gac ctg gcc gct ctg agc gtc agg gga gga tgc tgt tcc	40	144
Lys Arg Ser Asp Leu Ala Ala Leu Ser Val Arg Gly Gly Cys Cys Ser		
35	40	45

cat cct gcc tgt gcg gtg aat cat cca gag ctt tgt ggc tgaagacgct	55	193
His Pro Ala Cys Ala Val Asn His Pro Glu Leu Cys Gly		
50	55	60

gatgccccag gaccctctga accacgacgt 223

<210> 107
<211> 61
<212> PRT
<213> Conus betulinus

<400> 107
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Gly Arg Ala Phe Arg Gly Arg Asn Arg Ala Ala Asp Asp	25	20
20	25	30

Lys Arg Ser Asp Leu Ala Ala Leu Ser Val Arg Gly Gly Cys Cys Ser	40	35
35	40	45

His Pro Ala Cys Ala Val Asn His Pro Glu Leu Cys Gly	55	50
50	55	60

<210> 108
<211> 248
<212> DNA
<213> Conus betulinus

<220>
<221> CDS

<222> (1)..(180)

<400> 108

atg ttc acc gtc ttt ctg ttg gtc ttg gca acc act gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

ttc act tca ggt cgt gca tct ggt ggc agg aat gct gca gcc aaa gcg	96
Phe Thr Ser Gly Arg Ala Ser Gly Gly Arg Asn Ala Ala Ala Lys Ala	
20 25 30	

tct aac cgg atc gct atg gcc atc agc agt gga gca tgc tgt gca tat	144
Ser Asn Arg Ile Ala Met Ala Ile Ser Ser Gly Ala Cys Cys Ala Tyr	
35 40 45	

cct ccc tgt ttc gag gct tat cca gaa aga tgt ctg taacgtgaat	190
Pro Pro Cys Phe Glu Ala Tyr Pro Glu Arg Cys Leu	
50 55 60	

catccagacc tttgtggctg aagacgctga tgccccagga ccctctgaac cacgacgt	248
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<210> 109

<211> 60

<212> PRT

<213> Conus betulinus

<400> 109

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

Phe Thr Ser Gly Arg Ala Ser Gly Gly Arg Asn Ala Ala Lys Ala	
20 25 30	

Ser Asn Arg Ile Ala Met Ala Ile Ser Ser Gly Ala Cys Cys Ala Tyr	
35 40 45	

Pro Pro Cys Phe Glu Ala Tyr Pro Glu Arg Cys Leu	
50 55 60	

<210> 110

<211> 223

<212> DNA

<213> Conus betulinus

<220>

<221> CDS

<222> (1)..(192)

<400> 110

atg ttc acc gtc ttt ctg ttg gtc ttg gca acc act gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

ttc act tca gat cgt gca ttt cgt ggc agg aat tcc gca gcc aac gac	96
Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ser Ala Ala Asn Asp	
20 25 30	

aaa agg tct gac ctg gcc gct ctg agc gtc agg aga gga tgc tgc tcc	144
Lys Arg Ser Asp Leu Ala Ala Leu Ser Val Arg Arg Gly Cys Cys Ser	
35 40 45	

cat ccc gcc tgt agc gtg aat cat cca gag ctt tgt ggt aga aga cgc	192
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45

His Pro Ala Cys Ser Val Asn His Pro Glu Leu Cys Gly Arg Arg Arg		
50	55	60

tgtatgccccca ggaccctctg aaccacgacg t	223
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<210> 111
<211> 64
<212> PRT
<213> Conus betulinus

<400> 111
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ser Ala Ala Asn Asp
20 25 30

Lys Arg Ser Asp Leu Ala Ala Leu Ser Val Arg Arg Gly Cys Cys Ser
35 40 45

His Pro Ala Cys Ser Val Asn His Pro Glu Leu Cys Gly Arg Arg Arg		
50	55	60

<210> 112
<211> 248
<212> DNA
<213> Conus betulinus

<220>
<221> CDS
<222> (1)..(180)

<400> 112
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca ggt cgt gca tct ggt ggc agg aat gct gca gcc aaa gcg 96
Phe Thr Ser Gly Arg Ala Ser Gly Gly Arg Asn Ala Ala Ala Lys Ala
20 25 30

tct aac cgg atc gct ctg atc gtc agg aat gca gaa tgc tgg tat tat 144
Ser Asn Arg Ile Ala Leu Ile Val Arg Asn Ala Glu Cys Cys Tyr Tyr
35 40 45

cct ccc tgt tac gag gct tat cca gaa att tgt ctg taacgtgaat 190
Pro Pro Cys Tyr Glu Ala Tyr Pro Glu Ile Cys Leu
50 55 60

catccagacc tttgtggctg aagaccctga tgctccagga ccctctgaac cacgacgt 248

<210> 113
<211> 60
<212> PRT
<213> Conus betulinus

<400> 113
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Gly Arg Ala Ser Gly Gly Arg Asn Ala Ala Lys Ala

46

20	25	30
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Ser Asn Arg Ile Ala Leu Ile Val Arg Asn Ala Glu Cys Cys Tyr Tyr
 35 40 45

Pro Pro Cys Tyr Glu Ala Tyr Pro Glu Ile Cys Leu
 50 55 60

<210> 114

<211> 207

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(168)

<400> 114

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc att tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ile Ser	
1 5 10 15	

ttc act tca gat cgt gca tct gat ggc ggg aat gcc gca gcg tct gac	96
Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Ser Asp	
20 25 30	

ctg atc gct ctg acc atc aag gga tgc tgt tct cat cct ccc tgt gcc	144
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala	
35 40 45	

atg aat aat cca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga	198
Met Asn Asn Pro Asp Tyr Cys Gly	
50 55	

accacgacg

207

<210> 115

<211> 56

<212> PRT

<213> Conus pennaceus

<400> 115

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ile Ser	198
1 5 10 15	

Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Ser Asp	198
20 25 30	

Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala	198
35 40 45	

Met Asn Asn Pro Asp Tyr Cys Gly	198
50 55	

<210> 116

<211> 207

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(168)

<400> 116

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

ttc act tca gat cgt gca tct gat ggc ggg aat gcc gca atg tct gac	96
Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Met Ser Asp	
20 25 30	

ctg atc gct ctg acc atc aag gga tgc tgt tct cat cct ccc tgt ttc	144
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Phe	
35 40 45	

ctg aat aat cca gac tat tgt ggt tgacgacgct gatgctccag gaccctctga	198
Leu Asn Asn Pro Asp Tyr Cys Gly	
50 55	

accacgacg

207

<210> 117

<211> 56

<212> PRT

<213> Conus pennaceus

<400> 117

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Ala Met Ser Asp	
20 25 30	

Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Phe	
35 40 45	

Leu Asn Asn Pro Asp Tyr Cys Gly	
50 55	

<210> 118

<211> 210

<212> DNA

<213> Conus stercusmuscarum

<220>

<221> CDS

<222> (1)..(171)

<400> 118

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

ttc cct tca gat cgt gaa tct gat ggc gcg aat gac gaa gcc cgc acc	96
Phe Pro Ser Asp Arg Glu Ser Asp Gly Ala Asn Asp Glu Ala Arg Thr	
20 25 30	

gac gag cct gag gag cac gga ccg gac agg aat gga tgc tgt agg aat	144
Asp Glu Pro Glu Glu His Gly Pro Asp Arg Asn Gly Cys Cys Arg Asn	
35 40 45	

cct gcc tgt gag agc cac aga tgt ggt tgacgacgct gatgctccag	191
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Pro Ala Cys Glu Ser His Arg Cys Gly
 50 55

gaccctctga accacgacg 210

<210> 119
<211> 57
<212> PRT
<213> Conus stercusmuscarum

<400> 119
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Pro Ser Asp Arg Glu Ser Asp Gly Ala Asn Asp Glu Ala Arg Thr
 20 25 30

Asp Glu Pro Glu Glu His Gly Pro Asp Arg Asn Gly Cys Cys Arg Asn
 35 40 45

Pro Ala Cys Glu Ser His Arg Cys Gly
 50 55

<210> 120
<211> 210
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (1)...(180)

<400> 120
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc agc gac 96
Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ser Asp
 \ 20 25 30

aga gcg tct gac gcg gcc cac cag gga tgc tgt tcc aac cct gtc tgt 144
Arg Ala Ser Asp Ala Ala His Gln Gly Cys Cys Ser Asn Pro Val Cys
 35 40 45

cac gtg gaa cat cca gaa ctt tgt cgt aga aga cgc tgatgctcca 190
His Val Glu His Pro Glu Leu Cys Arg Arg Arg Arg
 50 55 60

ggaccctctg aaccacgacg 210

<210> 121
<211> 60
<212> PRT
<213> Conus circumcisus

<400> 121
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ser Asp

49

20	25	30
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Arg Ala Ser Asp Ala Ala His Gln Gly Cys Cys Ser Asn Pro Val Cys	35 40 45	
---	--	--

His Val Glu His Pro Glu Leu Cys Arg Arg Arg Arg	50 55 60	
---	--	--

<210> 122

<211> 213

<212> DNA

<213> Conus circumcisus

<220>

<221> CDS

<222> (1)...(174)

<400> 122

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc	48	
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser		
1 5 10 15		

ttc cct tca aat cgt gaa tct gat ggc gcg aat gcc gaa gtc cgc acc	96	
Phe Pro Ser Asn Arg Glu Ser Asp Gly Ala Asn Ala Glu Val Arg Thr		
20 25 30		

gac gag cct gag gag cac gac gaa ctg ggc ggg aat gga tgc tgt ggg	144	
Asp Glu Pro Glu Glu His Asp Glu Leu Gly Gly Asn Gly Cys Cys Gly		
35 40 45		

aat cct gac tgt acg agc cac agt tgt gat tgacgacgct gatgctccag	194	
Asn Pro Asp Cys Thr Ser His Ser Cys Asp		
50 55		

gaccctctga accacgacg	213	
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<210> 123

<211> 58

<212> PRT

<213> Conus circumcisus

<400> 123

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	88	
1 5 10 15		

Phe Pro Ser Asn Arg Glu Ser Asp Gly Ala Asn Ala Glu Val Arg Thr	194	
20 25 30		

Asp Glu Pro Glu Glu His Asp Glu Leu Gly Gly Asn Gly Cys Cys Gly	232	
35 40 45		

Asn Pro Asp Cys Thr Ser His Ser Cys Asp	270	
50 55		

<210> 124

<211> 207

<212> DNA

<213> Conus episcopatus

<220>

<221> CDS

50

<222> (1)..(168)

<400> 124

atg	ttc	acc	gtg	ttt	ctg	ttg	gtt	gtc	ttg	gca	acc	acc	gtc	gtt	tcc	48
Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser	
1				5					10				15			

ttc	act	tca	gat	cgt	gca	tct	gat	agc	agg	aag	gac	gca	gcg	tct	ggc	96
Phe	Thr	Ser	Asp	Arg	Ala	Ser	Asp	Ser	Arg	Lys	Asp	Ala	Ala	Ser	Gly	
					20			25				30				

ctg	atc	gct	ctg	acc	atc	aag	gga	tgc	tgt	tct	gat	cct	cgc	tgt	aac	144
Leu	Ile	Ala	Leu	Thr	Ile	Lys	Gly	Cys	Cys	Ser	Asp	Pro	Arg	Cys	Asn	
					35			40			45					

atg	aat	aat	cca	gac	tat	tgt	ggt	tgacgacgct	gatgctccag	gaccctctga	198
Met	Asn	Asn	Pro	Asp	Tyr	Cys	Gly				
			50		55						

accacgacg

207

<210> 125

<211> 56

<212> PRT

<213> Conus episcopatus

<400> 125

Met	Phe	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser
1				5					10				15		

Phe	Thr	Ser	Asp	Arg	Ala	Ser	Asp	Ser	Arg	Lys	Asp	Ala	Ala	Ser	Gly
					20			25			30				

Leu	Ile	Ala	Leu	Thr	Ile	Lys	Gly	Cys	Cys	Ser	Asp	Pro	Arg	Cys	Asn
					35			40			45				

Met	Asn	Asn	Pro	Asp	Tyr	Cys	Gly
			50		55		

<210> 126

<211> 213

<212> DNA

<213> Conus sponsalis

<220>

<221> CDS

<222> (1)..(174)

<400> 126

atg	tcc	acc	gtg	ttt	ctg	ttg	gtt	gtc	ctc	gca	acc	acc	gtc	gtt	tcc	48
Met	Ser	Thr	Val	Phe	Leu	Leu	Val	Val	Leu	Ala	Thr	Thr	Val	Val	Ser	
1				5					10				15			

ttc	act	gta	gat	cgt	gca	tct	gat	ggc	agg	gat	gtc	gca	atc	gac	gac	96
Phe	Thr	Val	Asp	Arg	Ala	Ser	Asp	Gly	Arg	Asp	Val	Ala	Ile	Asp	Asp	
					20			25			30					

aga	ttg	gtg	tct	ctc	cct	cag	atc	gcc	cat	gct	gac	tgt	tgt	tcc	gat	144
Arg	Leu	Val	Ser	Leu	Pro	Gln	Ile	Ala	His	Ala	Asp	Cys	Cys	Ser	Asp	
					35			40			45					

cct	gcc	tgc	aag	cag	acg	ccc	ggt	tgt	cgt	taaagacgct	gctgcctccag	194
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Pro Ala Cys Lys Gln Thr Pro Gly Cys Arg
 50 55

gaccctctga accacgacg 213

<210> 127
<211> 58
<212> PRT
<213> Conus sponsalis

<400> 127
Met Ser Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Val Asp Arg Ala Ser Asp Gly Arg Asp Val Ala Ile Asp Asp
 20 25 30

Arg Leu Val Ser Leu Pro Gln Ile Ala His Ala Asp Cys Cys Ser Asp
 35 40 45

Pro Ala Cys Lys Gln Thr Pro Gly Cys Arg
 50 55

<210> 128
<211> 221
<212> DNA
<213> Conus sponsalis ,

<220>
<221> CDS
<222> (1)...(168)

<400> 128
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gct tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ala Ser
 1 5 10 15

tgc att atc gat gat cca tct gat ggc agg aat att gca gtc gac gac 96
Phe Ile Ile Asp Asp Pro Ser Asp Gly Arg Asn Ile Ala Val Asp Asp
 20 25 30

aga ggg ctt ttc tct acg ctc ttc cat gct gat tgc tgt gaa aat cct 144
Arg Gly Leu Phe Ser Thr Leu Phe His Ala Asp Cys Cys Glu Asn Pro
 35 40 45

gcc tgt aga cac acg cag ggt tgt tgatcttgt tcttcaaaga cactgctggc 198
Ala Cys Arg His Thr Gln Gly Cys
 50 55

ccaggaccct ctgaaccacg acg 221

<210> 129
<211> 56
<212> PRT
<213> Conus sponsalis

<400> 129
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Ala Ser
 1 5 10 15

Phe Ile Ile Asp Asp Pro Ser Asp Gly Arg Asn Ile Ala Val Asp Asp

52

20	25	30
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Arg Gly Leu Phe Ser Thr Leu Phe His Ala Asp Cys Cys Glu Asn Pro	40	45
35		
Ala Cys Arg His Thr Gln Gly Cys		
50	55	

<210> 130
<211> 220
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)...(180)

<400> 130
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca gat cgt gca ttt cgt ggc agg aat gcc gca gcc aaa gag	20	96
Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys Glu		
25	30	

tct ggc ctg gtc ggt ctg acc gac aag acg cga gga tgc tgt tct cat	35	144
Ser Gly Leu Val Gly Leu Thr Asp Lys Thr Arg Gly Cys Cys Ser His		
40	45	

cct gcc tgt aac gta gat cat cca gaa att tgt ggt tgaagacgct	50	190
Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Gly		
55	60	

gatgctccag gaccctctga accacgacgt 220

<210> 131
<211> 60
<212> PRT
<213> Conus dalli

<400> 131
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys Glu	20	25
25	30	

Ser Gly Leu Val Gly Leu Thr Asp Lys Thr Arg Gly Cys Cys Ser His	35	45
35	40	

Pro Ala Cys Asn Val Asp His Pro Glu Ile Cys Gly	50	60
50	55	

<210> 132
<211> 208
<212> DNA
<213> Conus dalli

<220>
<221> CDS

<222> (1)..(177)

<400> 132

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Ala Thr Thr Val Val Ser	
1 5 10 15	

ttc act tca gat ggt gca tct gat gac agg aaa gcc gct gcg tct gac	96
Phe Thr Ser Asp Gly Ala Ser Asp Asp Arg Lys Ala Ala Ser Asp	
20 25 30	

ctg atc act ctg acc atc aag gga tgc tgt tct cgt cct ccc tgt atc	144
Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile	
35 40 45	

gcg aat aat cca gac ttg tgt ggt cga cga cgc tgatgctcca ggaccctctg	197
Ala Asn Asn Pro Asp Leu Cys Gly Arg Arg Arg	
50 55	

aaccacgacg :	208
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<210> 133

<211> 59

<212> PRT

<213> Conus dalli

<400> 133

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser	
1 5 10 15	

Phe Thr Ser Asp Gly Ala Ser Asp Asp Arg Lys Ala Ala Ser Asp	
20 25 30	

Leu Ile Thr Leu Thr Ile Lys Gly Cys Cys Ser Arg Pro Pro Cys Ile	
35 40 45	

Ala Asn Asn Pro Asp Leu Cys Gly Arg Arg Arg	
50 55	

<210> 134

<211> 223

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (1)..(192)

<400> 134

atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc	48
Met Phe Thr Val Phe Leu Leu Val Val Ala Thr Thr Val Val Ser	
1 5 10 15	

tcc act tca ggt cgt cgt gca ttt cat ggc agg aat gcc gca gcc aaa	96
Ser Thr Ser Gly Arg Arg Ala Phe His Gly Arg Asn Ala Ala Ala Lys	
20 25 30	

gcg tct gga ctg gtc ggt ctg act gac agg aga cca caa tgc tgt agt	144
Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser	
35 40 45	

gat cct cgc tgt aac gta ggt cat cca gaa ctt tgt ggt gga aga cgc	192
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54

Asp Pro Arg Cys Asn Val Gly His Pro Glu Leu Cys Gly Gly Arg Arg
 50 55 60

tgatgctcca ggaccctctg aaccacaacg t 223

<210> 135
 <211> 64
 <212> PRT
 <213> Conus dalli

<400> 135
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ser Thr Ser Gly Arg Arg Ala Phe His Gly Arg Asn Ala Ala Lys
 20 25 30

Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Gln Cys Cys Ser
 35 40 45

Asp Pro Arg Cys Asn Val Gly His Pro Glu Leu Cys Gly Gly Arg Arg
 50 55 60

<210> 136
 <211> 220
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (1)...(189)

<400> 136
 atg ttc acc gtc ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

tcc act tca ggt cgt gca ttt cat ggc agg aat gcc gca gcc aaa gcg 96
 Ser Thr Ser Gly Arg Ala Phe His Gly Arg Asn Ala Ala Lys Ala
 20 25 30

tct ggc ctg gtc ggt ctg acc gac aag agg caa gta tgc tgt agt gat 144
 Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Val Cys Cys Ser Asp
 35 40 45

cct cgc tgt aac gta ggt cat cca gaa att tgt ggt gga aga cgc 189
 Pro Arg Cys Asn Val Gly His Pro Glu Ile Cys Gly Gly Arg Arg
 50 55 60

tgatgctcca ggaccctctg aaccacgacg t 220

<210> 137
 <211> 63
 <212> PRT
 <213> Conus dalli

<400> 137
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ser Thr Ser Gly Arg Ala Phe His Gly Arg Asn Ala Ala Lys Ala

55

20

25

30

Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Val Cys Cys Ser Asp
 35 40 45

Pro Arg Cys Asn Val Gly His Pro Glu Ile Cys Gly Gly Arg Arg
 50 55 60

<210> 138

<211> 208

<212> DNA

<213> Conus achatinus

<220>

<221> CDS

<222> (1)..(180)

<400> 138

atg ttc acc gtg ttt ctg ttg gtt gtc ttg aca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser
 1 5 10 15

tgc cct tca gat agt gca tct ggt ggc agg gat gac gag gcc aaa gac 96
 Phe Pro Ser Asp Ser Ala Ser Gly Gly Arg Asp Asp Glu Ala Lys Asp
 20 25 30

gaa agg tct gac atg tac gaa ttg aaa cgg aat gga cgc tgt tgc cat 144
 Glu Arg Ser Asp Met Tyr Glu Leu Lys Arg Asn Gly Arg Cys Cys His
 35 40 45

cct gcc tgt ggt ggc aaa tac gtt aaa tgt gga cgc tgc tgatgctcca 190
 Pro Ala Cys Gly Gly Lys Tyr Val Lys Cys Gly Arg
 50 55 60

ggaccctctc gaaccacg 208

<210> 139

<211> 60

<212> PRT

<213> Conus achatinus

<400> 139

Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser
 1 5 10 15

Phe Pro Ser Asp Ser Ala Ser Gly Gly Arg Asp Asp Glu Ala Lys Asp
 20 25 30

Glu Arg Ser Asp Met Tyr Glu Leu Lys Arg Asn Gly Arg Cys Cys His
 35 40 45

Pro Ala Cys Gly Gly Lys Tyr Val Lys Cys Gly Arg
 50 55 60

<210> 140

<211> 211

<212> DNA

<213> Conus bullatus

<220>

<221> CDS

<222> (1)...(174)

<400> 140
atg ttc acc gcg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc tct aca gat gat gaa tct gat ggc tcg aat gaa gaa ccc agc gcc 96
Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala
20 25 30

gac cag act gcc agg tcc tca atg aac agg gcg cct gga tgc tgt aac 144
Asp Gln Thr Ala Arg Ser Ser Met Asn Arg Ala Pro Gly Cys Cys Asn
35 40 45

aat cct gcc tgt gtg aag cac aga tgt gga tgacgctgat gctccaggac 194
Asn Pro Ala Cys Val Lys His Arg Cys Gly
50 55

cctctgaacc acgacgt 211

<210> 141
<211> 58
<212> PRT
<213> Conus bullatus

<400> 141
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser 15
1 5 10 15

Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala
20 25 30

Asp Gln Thr Ala Arg Ser Ser Met Asn Arg Ala Pro Gly Cys Cys Asn
35 40 45

Asn Pro Ala Cys Val Lys His Arg Cys Gly
50 55

<210> 142
<211> 214
<212> DNA
<213> Conus bullatus

<220>
<221> CDS
<222> (1)...(177)

<400> 142
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc tct aca gat gat gaa tct gat ggc tcg aat gaa gaa ccc agc gcc 96
Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala
20 25 30

gac cag gct gcc agg tcc gca atg aac agg ccg cct gga tgc tgt aac 144
Asp Gln Ala Ala Arg Ser Ala Met Asn Arg Pro Pro Gly Cys Cys Asn
35 40 45

aat cct gcc tgt gtg aag cac aga tgt ggt gga tgacgctgat gctccaggac 197

Asn Pro Ala Cys Val Lys His Arg Cys Gly Gly
50 55

cctctgaacc acgacgt 214

<210> 143
<211> 59
<212> PRT
<213> Conus bullatus

<400> 143
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Ser Thr Asp Asp Glu Ser Asp Gly Ser Asn Glu Glu Pro Ser Ala
20 25 30

Asp Gln Ala Ala Arg Ser Ala Met Asn Arg Pro Pro Gly Cys Cys Asn
35 40 45

Asn Pro Ala Cys Val Lys His Arg Cys Gly Gly
50 55

<210> 144
<211> 208
<212> DNA
<213> Conus bullatus

<220>
<221> CDS
<222> (1)..(177)

<400> 144
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

tgc cct tca gat cgt gac tct gat ggc gcg gat gcc gaa gcc agt gac 96
Phe Pro Ser Asp Arg Asp Ser Asp Gly Ala Asp Ala Glu Ala Ser Asp
20 25 30

gag cct gtt gag ttc gaa agg gac gag aat gga tgc tgt tgg aat cct 144
Glu Pro Val Glu Phe Arg Asp Glu Asn Gly Cys Cys Trp Asn Pro
35 40 45

tcc tgt ccg agg ccc aga tgt aca gga cga cgc taatgctcca ggaccctctg 197
Ser Cys Pro Arg Pro Arg Cys Thr Gly Arg Arg
50 55

aaccacgacg t 208

<210> 145
<211> 59
<212> PRT
<213> Conus bullatus

<400> 145
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Pro Ser Asp Arg Asp Ser Asp Gly Ala Asp Ala Glu Ala Ser Asp

20	25	30
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Glu Pro Val Glu Phe Glu Arg Asp Glu Asn Gly Cys Cys Trp Asn Pro	35 40 45	
---	--	--

Ser Cys Pro Arg Pro Arg Cys Thr Gly Arg Arg	50 55	
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<210> 146

<211> 211

<212> DNA

<213> Conus bullatus

<220>

<221> CDS

<222> (1)..(180)

<400> 146

atg ttc acc gtg ttt ctg ttg gtc ttg aca acc act gtc gtt tcc	48	
Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser		
1 5 10 15		

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac	96	
Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp		
20 25 30		

aaa gcg tct gac gtg gtc acg ctg gtc ctc aag gga tgc tgt tcc acc	144	
Lys Ala Ser Asp Val Val Thr Leu Val Leu Lys Gly Cys Cys Ser Thr		
35 40 45		

cct ccc tgt gct gtg ctg tat tgt ggt aga aga cgc tgatgctcca	190	
Pro Pro Cys Ala Val Leu Tyr Cys Gly Arg Arg Arg		
50 55 60		

ggaccctctg aaccacgacg t	211	
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<210> 147

<211> 60

<212> PRT

<213> Conus bullatus

<400> 147

Met Phe Thr Val Phe Leu Leu Val Val Leu Thr Thr Thr Val Val Ser	147	
1 5 10 15		

Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp	147	
20 25 30		

Lys Ala Ser Asp Val Val Thr Leu Val Leu Lys Gly Cys Cys Ser Thr	147	
35 40 45		

Pro Pro Cys Ala Val Leu Tyr Cys Gly Arg Arg Arg	147	
50 55 60		

<210> 148

<211> 212

<212> DNA

<213> Conus distans

<220>

<221> CDS

59

<222> (1)..(171)

<400> 148

atg ttc acc gtc ttt ctg ttg gtt gtc ttc gca tcc tct gtc acc tta	48
Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu	
1 5 10 15	

gat cgt gca tct tat ggc agg tat gcc tca ccc gtc gac aga gcg tct	96
Asp Arg Ala Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser	
20 25 30	

gcc ctg atc gct cag gcc atc ctt cga gat tgc tgc tcc aat cct cct	144
Ala Leu Ile Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro	
35 40 45	

tgt gcc cat aat aat cca gac tgt cgt taaagacgct gcttgctcca	191
Cys Ala His Asn Asn Pro Asp Cys Arg	
50 55	

ggaccctctg aaccacgacg t	212
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<210> 149

<211> 57

<212> PRT

<213> Conus distans

<400> 149

Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu	
1 5 10 15	

Asp Arg Ala Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser	
20 25 30	

Ala Leu Ile Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro	
35 40 45	

Cys Ala His Asn Asn Pro Asp Cys Arg	
50 55	

<210> 150

<211> 63

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (1)..(60)

<400> 150

gga tgc tgt tct aat cct ccc tgt atc gcg aag aat cca cac atg tgt	48
Gly Cys Cys Ser Asn Pro Pro Cys Ile Ala Lys Asn Pro His Met Cys	
1 5 10 15	

ggt gga aga cgc tga	63
Gly Gly Arg Arg	
20	

<210> 151

<211> 20

<212> PRT

<213> Conus textile

60

<400> 151
Gly Cys Cys Ser Asn Pro Pro Cys Ile Ala Lys Asn Pro His Met Cys
1 5 10 15

Gly Gly Arg Arg
20

<210> 152
<211> 220
<212> DNA
<213> Conus consors

<220>
<221> CDS
<222> (1)..(189)

<400> 152
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc cct tca gat cgt gca tct gat ggc agg aat gcc gca gcc aac gac 96
Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp
20 25 30

aaa gcg tct gac gtg atc acg ctg gcc ctc aag gga tgc tgt tcc aac 144
Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn
35 40 45

cct gtc tgt cac ttg gag cat tca aac ctt tgt ggt aga aga cgc 189
Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg
50 55 60

tgatgctcca ggaccctctg aaccacgacg t 220

<210> 153
<211> 63
<212> PRT
<213> Conus consors

<400> 153
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Asn Asp
20 25 30

Lys Ala Ser Asp Val Ile Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn
35 40 45

Pro Val Cys His Leu Glu His Ser Asn Leu Cys Gly Arg Arg Arg
50 55 60

<210> 154
<211> 15
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (4)..(12)

<223> Xaa at residues 4, 11 and 12 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr. Xaa at residue 6 is Pro or hydroxy-Pro.

<220>

<221> PEPTIDE

<222> (9)..(15)

<223> Xaa at residues 9, 10 and 15 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at residue 14 is Trp (D or L) or halo-Trp.

<400> 154

Gly	Cys	Cys	Xaa	Asn	Xaa	Val	Cys	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa
1					5				10					15

<210> 155

<211> 16

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(3)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 3 and 9 is Pro or hydroxy-Pro.

<220>

<221> PEPTIDE

<222> (13)

<223> Xaa at residue 13 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 155

Xaa	Xaa	Xaa	Gly	Cys	Cys	Arg	His	Xaa	Ala	Cys	Gly	Xaa	Asn	Arg	Cys
1					5				10					15	

<210> 156

<211> 13

<212> PRT

<213> Conus musicus

<220>

<221> PEPTIDE

<222> (5)..(11)

<223> Xaa at residues 5 and 11 is Pro or hydroxy-Pro.

<400> 156

Cys	Gys	Ala	Asp	Xaa	Asp	Cys	Arg	Phe	Arg	Xaa	Gly	Cys
1					5				10			

<210> 157

<211> 17

<212> PRT

<213> Conus musicus

<220>

<221> PEPTIDE

<222> (4)..(13)

<223> Xaa at residues 4 and 13 is Tyr, nor-Tyr,

mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr or nitro-Tyr; Xaa at residues 6 and
10 is Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (9)..(17)
<223> Xaa at residues 9 and 16 is Trp (D or L) or
halo-Trp; Xaa at residues 11 and 17 is Lys,
N-methyl-Lys, N,N-dimethyl-Lys or
N,N,N-trimethyl-Lys.

<400> 157
Gly Cys Cys Xaa Asn Xaa Ser Cys Xaa Xaa Xaa Thr Xaa Cys Ser Xaa
1 5 10 15

Xaa

<210> 158
<211> 13
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (5)..(8)
<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at
residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys
or N,N,N-trimethyl-Lys.

<220>
<221> PEPTIDE
<222> (9)..(11)
<223> Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa
at residue 11 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 158
Cys Cys Ser Asn Xaa Thr Cys Xaa Xaa Thr Xaa Gly Cys
1 5 10

<210> 159
<211> 13
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (5)..(11)
<223> Xaa at residues 5 and 11 is Pro or hydroxy-Pro;
Xaa at residue 8 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 159
Cys Cys Ala Asn Xaa Ile Cys Xaa Asn Thr Xaa Gly Cys
1 5 10

<210> 160
<211> 13

<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (5)..(8)
<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>
<221> PEPTIDE
<222> (9)..(11)
<223> Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa at residue 11 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 160
Cys Cys Asn Asn Xaa Thr Cys Xaa Xaa Thr Xaa Gly Cys
1 5 10

<210> 161
<211> 13
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (5)..(8)
<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>
<221> PEPTIDE
<222> (9)..(11)
<223> Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa at residue 11 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 161
Cys Cys Ser Asn Xaa Val Cys Xaa Xaa Thr Xaa Gly Cys
1 5 10

<210> 162
<211> 17
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (15)
<223> Xaa at residue 15 is Lys, N-methyl-Lys,

N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 162
Gly Gly Cys Cys Ser Xaa Xaa Xaa Cys Ile Ala Ser Asn Xaa Xaa Cys
1 5 10 15
Gly

<210> 163
<211> 15
<212> PRT
<213> Conus lividus

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 163
Gly Cys Cys Ser His Xaa Val Cys Ser Ala Met Ser Xaa Ile Cys
1 5 10 15

<210> 164
<211> 15
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (4)..(12)
<223> Xaa at residues 4 and 12 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at
residue 6 is Pro or hydroxy-Pro.

<220>
<221> PEPTIDE
<222> (7)..(14)
<223> Xaa at residues 7 and 14 is Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 164
Gly Cys Cys Xaa Asn Xaa Xaa Cys Gly Ala Ser Xaa Thr Xaa Cys
1 5 10 15

<210> 165
<211> 15
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (5)..(13)
<223> Xaa at residue 5 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr; Xaa at residues 6, 7 and 13 is Pro or
hydroxy-Pro.

<400> 165
Gly Cys Cys Ser Xaa Xaa Xaa Cys Phe Ala Thr Asn Xaa Asp Cys

65

1

5

10

15

<210> 166
<211> 17
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr; Xaa at residues 7, 8 and 14 is Pro or
hydroxy-Pro.

<400> 166
Gly Gly Cys Cys Ser Xaa Xaa Xaa Cys Ile Ala Asn Asn Xaa Leu Cys
1, 5 10 15

Ala

<210> 167
<211> 17
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (6)..(14)
<223> Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr; Xaa at residues 7, 8 and 14 is Pro or
hydroxy-Pro.

<400> 167
Gly Gly Cys Cys Ser Xaa Xaa Xaa Cys Ile Ala Asn Asn Xaa Phe Cys
1 5 10 15

Ala

<210> 168
<211> 16
<212> PRT
<213> Conus virgo

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro.

<400> 168
Asp Cys Cys Ser Asn Xaa Xaa Cys Ser Gln Asn Asn Xaa Asp Cys Met
1 5 10 15

<210> 169
<211> 16
<212> PRT
<213> Conus virgo

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro.

<400> 169
Asp Cys Cys Ser Asn Xaa Xaa Cys Ala His Asn Asn Xaa Asp Cys Arg
1 5 10 15

<210> 170
<211> 20
<212> PRT
<213> Conus achatinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residues 1, 11 and 14 is Glu or
gamma-carboxy-Glu; Xaa at residue 6 is Pro or
hydroxy-Pro.

<400> 170
Xaa Cys Cys Thr Asn Xaa Val Cys His Ala Xaa His Gln Xaa Leu Cys
1 5 10 15

Ala Arg Arg Arg
20

<210> 171
<211> 16
<212> PRT
<213> Conus achatinus

<220>
<221> PEPTIDE
<222> (6)..(10)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at
residue 10 is Glu or gamma-carboxy-Glu.

<400> 171
Gly Cys Cys Ser Asn Xaa Val Cys His Leu Xaa His Ser Asn Leu Cys
1 5 10 15

<210> 172
<211> 20
<212> PRT
<213> Conus achatinus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residues 1, 11 and 14 is Glu or
gamma-carboxy-Glu; Xaa at residue 6 is Pro or
hydroxy-Pro.

<400> 172
Xaa Cys Cys Thr Asn Xaa Val Cys His Val Xaa His Gln Xaa Leu Cys
1 5 10 15

Ala Arg Arg Arg
20

<210> 173
<211> 17
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<220>
<221> PEPTIDE
<222> (7)..(14)
<223> Xaa at residues 7 and 14 is Pro or hydroxy-Pro.

<400> 173
Xaa Xaa Cys Cys Ser Xaa Xaa Ala Cys Asn Leu Asp His Xaa Xaa Leu
1 5 10 15

Cys

<210> 174
<211> 18
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro; Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu.

<400> 174
Xaa Xaa Cys Cys Ser Asp Xaa Arg Cys Asn Ser Thr His Xaa Xaa Leu
1 5 10 15

Cys Gly

<210> 175
<211> 21
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (7)..(12)
<223> Xaa at residues 7 and 8 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or halo-Trp; Xaa at residues 11 and 12 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>
<221> PEPTIDE
<222> (13)..(19)

<223> Xaa at residue 13 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr ; Xaa at residue 19 is Glu or gamma-carboxy-Glu.

<400> 175
Leu Asn Cys Cys Met Ile Xaa Xaa Cys Xaa Xaa Xaa Gly Asp Arg
1 5 10 15
Cys Ser Xaa Val Arg
20

<210> 176

<211> 22

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (9)..(20)

<223> Xaa at residue 9 is Pro or hydroxy-Pro; Xaa at residues 12 and 20 is Glu or gamma-carboxy-Glu; Xaa at residue 14 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 176

Ala Phe Gly Cys Cys Asp Leu Ile Xaa Cys Leu Xaa Arg Xaa Gly Asn
1 5 10 15

Arg Cys Asn Xaa Val His
20

<210> 177

<211> 21

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (8)..(16)

<223> Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or halo-Trp; Xaa at residues 12 and 16 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>

<221> PEPTIDE

<222> (11)..(19)

<223> Xaa at residues 11 and 19 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 177

Leu Gly Cys Cys Asn Val Thr Xaa Cys Xaa Xaa Xaa Gly Asp Xaa
1 5 10 15

Cys Asn Xaa Val Arg
20

<210> 178
<211> 20
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (2)..(14)
<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 7 and 14 is Pro or hydroxy-Pro.

<400> 178
Asp Xaa Cys Cys Ser Asn Xaa Ala Cys Arg Val Asn Asn Xaa His Val
1 5 10 15

Cys Arg Arg Arg
20

<210> 179
<211> 21
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (7)..(12)
<223> Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or halo-Trp; Xaa at residue 12 is Glu or gamma-carboxy-Glu.

<220>
<221> PEPTIDE
<222> (13)..(19)
<223> Xaa at residue 13 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; Xaa at residues 14 and 19 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 179
Leu Asn Cys Cys Ser Ile Xaa Gly Cys Xaa Asn Xaa Xaa Asp Arg
1 5 10 15

Cys Ser Xaa Val Arg
20

<210> 180
<211> 18
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (7)..(14)
<223> Xaa at residues 7 and 14 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 180
Gly Gly Cys Cys Ser His Xaa Val Cys Xaa Phe Asn Asn Xaa Gln Met
1 5 10 15

70

Cys Arg

<210> 181
<211> 18
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (7)..(14)
<223> Xaa at residues 7 and 14 is Pro or hydroxy-Pro.

<400> 181
Gly Gly Cys Cys Ser His Xaa Val Cys Asn Leu Asn Asn Xaa Gln Met
1 5 10 15

Cys Arg

<210> 182
<211> 17
<212> PRT
<213> Conus bandanus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa
at residues 9 and 15 is Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 182
Gly Cys Cys Ser His Xaa Xaa Cys Xaa Ala Asn Asn Gln Ala Xaa Cys
1 5 10 15

Asn

<210> 183
<211> 17
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (7)..(15)
<223> Xaa at residues 7 and 14 is Pro and hydroxy-Pro;
Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 183
Gly Gly Cys Cys Ser His Xaa Ala Cys Ser Val Thr His Xaa Xaa Leu
1 5 10 15

Cys

<210> 184
<211> 18

<212> PRT
 <213> Conus betulinus

 <220>
 <221> PEPTIDE
 <222> (6)..(12)
 <223> Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
 nitro-Tyr; Xaa at residue 7 is Pro and
 hydroxy-Pro; Xaa at residue 12 is Glu or
 gamma-carboxy-Glu.

 <400> 184
 Gly Gly Cys Cys Ser Xaa Xaa Ala Cys Ser Val Xaa His Gln Asp Leu
 1 5 10 15

 Cys Asp

<210> 185
 <211> 25
 <212> PRT
 <213> Conus characteristicus

 <220>
 <221> PEPTIDE
 <222> (8)..(22)
 <223> Xaa at residues 8 and 22 is Pro or hydroxy-Pro;
 Xaa at residue 10 is Trp (D or L) or halo-Trp; Xaa
 at residue 13 is Tyr, nor-Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
 nitro-Tyr.

 <220>
 <221> PEPTIDE
 <222> (15)..(19)
 <223> Xaa at residues 15, 16 and 19 is Glu or
 gamma-carboxy-Glu.

 <400> 185
 Val Ser Cys Cys Val Val Arg Xaa Cys Xaa Ile Arg Xaa Gln Xaa Xaa
 1 5 10 15

Cys Leu Xaa Ala Asp Xaa Arg Thr Leu
 20 25

<210> 186
 <211> 21
 <212> PRT
 <213> Conus characteristicus

 <220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at
 residue 7 is Pro or hydroxy-Pro; Xaa at residue 10
 is Trp (D or L) or halo-Trp; Xaa at residues 11
 and 19 is Glu or gamma-carboxy-Glu.

 <220>
 <221> PEPTIDE
 <222> (12)..(16)

<223> Xaa at residues 12 and 16 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at residue 13 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 186
Xaa Asn Cys Cys Ser Ile Xaa Gly Cys Xaa Xaa Xaa Xaa Gly Asp Xaa
1 5 10 15
Cys Ser Xaa Val Arg
20

<210> 187

<211> 16

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (6)...(13)

<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 11 is Glu or gamma-carboxy-Glu.

<400> 187

Gly Cys Cys Ser Asn Xaa Val Cys His Leu Xaa His Xaa Asn Ala Cys
1 5 10 15

<210> 188

<211> 17

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (6)...(13)

<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 9 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 188

Gly Cys Cys Ser Asn Xaa Ile Cys Xaa Phe Asn Asn Xaa Arg Ile Cys
1 5 10 15

Arg

<210> 189

<211> 17

<212> PRT

<213> Conus episcopatus

<220>

<221> PEPTIDE

<222> (1)...(14)

<223> Xaa at residues 1 and 14 is Glu or
gamma-carboxy-Glu; Xaa at residues 6, 7 and 13 is
Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or
L) or halo-Trp.

<220>

<221> PEPTIDE
<222> (11)
<223> Xaa at residue 11 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 189
Xaa Cys Cys Ser Gln Xaa Xaa Cys Arg Xaa Xaa His Xaa Xaa Leu Cys
1 5 10 15

Ser

<210> 190
<211> 16
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (6)
<223> Xaa at residue 6 is Pro or hydroxy-Pro.

<400> 190
Gly Cys Cys Ser His Xaa Ala Cys Ala Gly Asn Asn Gln His Ile Cys
1 5 10 15

<210> 191
<211> 18
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 191
Gly Cys Cys Ala Val Xaa Ser Cys Arg Leu Arg Asn Xaa Asp Leu Cys
1 5 10 15

Gly Gly

<210> 192
<211> 16
<212> PRT
<213> Conus imperialis

<220>
<221> NP_BIND
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 192
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
1 5 10 15

<210> 193
<211> 20
<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (2)..(10)

<223> Xaa at residues 2, 7, 9 and 10 is Pro or hydroxy-Pro; Xaa at residues 3 and 4 is Glu or gamma-carboxy-Glu.

<400> 193

Thr Xaa Xaa Xaa Cys Cys Xaa Asn Xaa Xaa Cys Phe Ala Thr Asn Ser
1 5 10 15

Asp Ile Cys Gly
20

<210> 194

<211> 17

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (7)..(12)

<223> Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 12 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 194

Asp Ala Cys Cys Ser Asp Xaa Arg Cys Ser Gly Xaa His Gln Asp Leu
1 5 10 15

Cys

<210> 195

<211> 17

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (1)..(7)

<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Pro or hydroxy-Pro.

<400> 195

Xaa Asp Cys Cys Ser Asp Xaa Arg Cys Ser Val Gly His Gln Asp Leu
1 5 10 15

Cys

<210> 196

<211> 16

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (6)

<223> Xaa at residue 6 is Pro or hydroxy-Pro.

<400> 196

Gly Cys Cys Ser His Xaa Ala Cys Ala Gly Ser Asn Ala His Ile Cys
1 5 10 15

<210> 197

<211> 17

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (1)..(7)

<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa
at residue 7 is Pro or hydroxy-Pro.

<400> 197

Xaa Asp Cys Cys Ser Asp Xaa Arg Cys Ser Val Gly His Gln Asp Met
1 5 10 15

Cys

<210> 198

<211> 16

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (6)..(13)

<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 198

Gly Cys Cys Ser His Xaa Ala Cys Ala Gly Asn Asn Xaa His Ile Cys
1 5 10 15

<210> 199

<211> 17

<212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (6)..(14)

<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 199

Gly Cys Cys Gly Asn Xaa Ser Cys Ser Ile His Ile Xaa Xaa Val Cys
1 5 10 15

Asn

<210> 200

<211> 21

<212> PRT
<213> Conus lividus

<220>
<221> PEPTIDE
<222> (4)..(5)
<223> Xaa at residues 4 and 5 is Glu or gamma-carboxy-Glu.

<400> 200
Thr Asp Ser Xaa Xaa Cys Cys Leu Asp Ser Arg Cys Ala Gly Gln His
1 5 10 15

Gln Asp Leu Cys Gly
20

<210> 201
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 9 and 15 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 201
Gly Cys Cys Ser Asn Xaa Xaa Cys Xaa Ala Asn Asn Gln Ala Xaa Cys
1 5 10 15

Asn

<210> 202
<211> 16
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 202
Gly Cys Cys Ser His Xaa Ala Cys Ser Val Asn Asn Xaa Asp Ile Cys
1 5 10 15

<210> 203
<211> 18
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (2)..(15)
<223> Xaa at residues 2 and 12 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at residue 14 is Pro or hydroxy-Pro.

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<220>
<221> PEPTIDE
<222> (16)
<223> Xaa at residue 16 is Tyr, mono-halo-Tyr,
      di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
      nitro-Tyr.

<400> 203
Gly Xaa Cys Cys Ile Asn Asp Ala Cys Arg Ser Xaa His Xaa Gln Xaa
     1           5           10          15

Cys Ser

<210> 204
<211> 17
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (4)..(15)
<223> Xaa at residues 4 and 15 is Tyr, nor-Tyr,
      mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
      O-phospho-Tyr or nitro-Tyr; Xaa at residue 13 is
      Pro or hydroxy-Pro.

<400> 204
Gly Cys Cys Xaa Asn Ile Ala Cys Arg Ile Asn Asn Xaa Arg Xaa Cys
     1           5           10          15

Arg

<210> 205
<211> 17
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
      Xaa at residues 12 and 15 is Tyr, nor-Tyr,
      mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
      O-phospho-Tyr or nitro-Tyr.

<220>
<221> PEPTIDE
<222> (14)
<223> Xaa at residue 14 is Lys, N-methyl-Lys,
      N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 205
Gly Cys Cys Ser His Xaa Val Cys Arg Phe Asn Xaa Xaa Xaa Xaa Cys
     1           5           10          15

Gly

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<210> 206

<211> 18
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (2)..(15)
<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr

<400> 206
Asp Xaa Cys Cys Ala Ser Xaa Xaa Cys Arg Leu Asn Asn Xaa Xaa Val
1 5 10 15

Cys His

<210> 207
<211> 19
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (6)..(18)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 9 is Trp (D or L) or halo-Trp; Xaa at residues 14 and 18 is Glu or gamma-carboxy-Glu.

<220>
<221> PEPTIDE
<222> (15)
<223> Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 207
Gly Cys Cys Ser Asn Xaa Val Cys Xaa Gln Asn Asn Ala Xaa Xaa Cys
1 5 10 15

Arg Xaa Ser

<210> 208
<211> 16
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 208
Gly Cys Cys Ser His Xaa Xaa Cys Ala Gln Asn Asn Gln Asp Xaa Cys
1 5 10 15

<210> 209
 <211> 19
 <212> PRT
 <213> Conus obscurus

<220>
 <221> PEPTIDE
 <222> (6)..(15)
 <223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residues 14 and 18 is Glu or gamma-carboxy-Glu; Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<400> 209
 Gly Cys Cys Ser His Xaa Ala Cys Ser Gly Asn Asn Arg Xaa Xaa Cys
 1 5 10 15

Arg Xaa Ser

<210> 210
 <211> 18
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (2)..(15)
 <223> Xaa at residues 2, 7 and 14 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; Xaa at residue 15 is Glu or gamma-carboxy-Glu

<400> 210
 Asp Xaa Cys Cys Ser Xaa Xaa Asp Cys Gly Ala Asn His Xaa Xaa Ile
 1 5 10 15

Cys Gly

<210> 211
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residues 1 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or halo-Trp.

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 211
Xaa Cys Cys Ser Gln Xaa Xaa Cys Arg Xaa Xaa His Xaa Xaa Leu Cys
1 5 10 15

Ser

<210> 212
<211> 16
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 212
Gly Cys Cys Ser His Xaa Ala Cys Ala Gly Asn Asn Xaa His Ile Cys
1 5 10 15

<210> 213
<211> 16
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (6)..(15)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 15 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 213
Gly Cys Cys Ser Asp Xaa Ser Cys Asn Val Asn Asn Xaa Asp Xaa Cys
1 5 10 15

<210> 214
<211> 18
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(7)
<223> Xaa at residues 1 and 2 is Glu or
gamma-carboxy-Glu; Xaa at residue 7 is Pro or
hydroxy-Pro.

<400> 214
Xaa Xaa Cys Cys Ser Asp Xaa Arg Cys Ser Val Gly His Gln Asp Met
1 5 10 15

Cys Arg

<210> 215
<211> 17
<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (7)..(15)

<223> Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 15 is Glu or gamma-carboxy-Glu.

<400> 215

Gly Gly Cys Cys Ser Asn Xaa Ala Cys Leu Val Asn His Leu Xaa Met
1 5 10 15

Cys

<210> 216

<211> 18

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (3)..(15)

<223> Xaa at residues 3, 8 and 15 is Pro or hydroxy-Pro.

<400> 216

Arg Asp Xaa Cys Cys Phe Asn Xaa Ala Cys Asn Val Asn Asn Xaa Gln
1 5 10 15

Ile Cys

<210> 217

<211> 21

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (5)..(8)

<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp (D or L) or halo-Trp:

<400> 217

Cys Cys Ser Asp Xaa Ser Cys Xaa Arg Leu His Ser Leu Ala Cys Thr
1 5 10 15

Gly Ile Val Asn Arg
20

<210> 218

<211> 16

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (5)

<223> Xaa at residue 5 is Pro or hydroxy-Pro.

<400> 218

82

Cys Cys Thr Asn Xaa Ala Cys Leu Val Asn Asn Ile Arg Phe Cys Gly
1 5 10 15

<210> 219
<211> 18
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa
at residue 7 is Pro or hydroxy-Pro.

<400> 219
Asp Xaa Cys Cys Ser Asp Xaa Arg Cys His Gly Asn Asn Arg Asp His
1 5 10 15

Cys Ala

<210> 220
<211> 17
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 220
Asp Cys Cys Ser His Xaa Leu Cys Arg Leu Phe Val Xaa Gly Leu Cys
1 5 10 15

Ile

<210> 221
<211> 17
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 9 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>
<221> PEPTIDE
<222> (12)
<223> Xaa at residue 12 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr.

<400> 221
Gly Cys Cys Ser His Xaa Val Cys Xaa Val Arg Xaa Xaa Asp Leu Cys
1 5 10 15

Arg

<210> 222
<211> 16
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 222
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
1 5 10 15

<210> 223
<211> 16
<212> PRT
<213> Conus regius

<220>
<221> PEPTIDE
<222> (6)..(12)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at
residue 12 is Tyr, nor-Tyr, nor-Tyr,
mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
O-phospho-Tyr or nitro-Tyr.

<220>
<221> PEPTIDE
<222> (9)
<223> Xaa at residue 9 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 223
Gly Cys Cys Ser His Xaa Val Cys Xaa Val Arg Xaa Ser Asp Met Cys
1 5 10 15

<210> 224
<211> 17
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (7)..(14)
<223> Xaa at residues 7 and 14 is Pro or hydroxy-Pro;
Xaa at residue 10 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 224
Gly Gly Cys Cys Ser His Xaa Ala Cys Xaa Val His Phe Xaa His Ser
1 5 10 15

Cys

<210> 225

<211> 20
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (6)...(14)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro;
Xaa at residue 14 is Glu or gamma-carboxy-Glu.

<400> 225
Val Cys Cys Ser Asn Xaa Val Cys His Val Asp His Xaa Xaa Leu Cys
1 5 10 15
Arg Arg Arg Arg
20

<210> 226
<211> 17
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (6)...(13)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 226
Gly Cys Cys Ser His Xaa Val Cys Asn Leu Ser Asn Xaa Gln Ile Cys
1 5 10 15
Arg

<210> 227
<211> 18
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)...(15)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at
residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa
at residues 7 and 14 is Pro or hydroxy-Pro.

<400> 227
Xaa Xaa Cys Cys Ser His Xaa Ala Cys Asn Val Asp His Xaa Xaa Ile
1 5 10 15
Cys Arg

<210> 228
<211> 17
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (6)

<223> Xaa at residue 6 is Pro or hydroxy-Pro.

<400> 228

Gly Cys Cys Ser Asn Xaa Ala Cys Leu Val Asn His Ile Arg Phe Cys
1 5 10 15

Gly

<210> 229

<211> 17

<212> PRT

<213> Conus virgo

<220>

<221> PEPTIDE

<222> (6)..(13)

<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro.

<400> 229

Asp Cys Cys Asp Asp Xaa Ala Cys Thr Val Asn Asn Xaa Gly Leu Cys
1 5 10 15

Thr

<210> 230

<211> 20

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (6)..(13)

<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro;
Xaa at residue 11 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 230

Gly Cys Cys Ser Asn Xaa Xaa Cys Ile Ala Xaa Asn Xaa His Met Cys
1 5 10 15

Gly Gly Arg Arg
20

<210> 231

<211> 18

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (5)..(9)

<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at
residue 8 is Tyr, nor-Tyr, mono-halo-Tyr,
di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
nitro-Tyr; Xaa at residue 9 is Glu or
gamma-carboxy-Glu.

<220>

<221> PEPTIDE

<222> (10)..(14)
 <223> Xaa at residues 10, 11, 12 and 14 is Lys,
 N-methyl-Lys, N,N-dimethyl-Lys or
 N,N,N-trimethyl-Lys.

<400> 231
 Cys Cys Thr Ile Xaa Ser Cys Xaa Xaa Xaa Xaa Ile Xaa Ala Cys
 1 5 10 15
 Val Phe

<210> 232
 <211> 18
 <212> PRT
 <213> Conus regius

<220>
 <221> PEPTIDE
 <222> (6)..(16)
 <223> Xaa at residues 6 and 16 is Pro or hydroxy-Pro;
 Xaa at residue 13 is Lys, N-methyl-Lys,
 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 232
 Gly Cys Cys Gly Asn Xaa Ala Cys Ser Gly Ser Ser Xaa Asp Ala Xaa
 1 5 10 15
 Ser Cys

<210> 233
 <211> 108
 <212> DNA
 <213> Conus imperialis

<220>
 <221> CDS
 <222> (1)..(105)

<400> 233
 tct gat gga aag agt gcc gcg gcc aaa gcc aaa ccg tct cac ctg acg 48
 Ser Asp Gly Lys Ser Ala Ala Ala Lys Ala Lys Pro Ser His Leu Thr
 1 5 10 15
 gct cca ttc atc agg gac gaa tgc tgt tcc gat tct cgc tgt ggc aag 96
 Ala Pro Phe Ile Arg Asp Glu Cys Cys Ser Asp Ser Arg Cys Gly Lys
 20 25 30
 aac tgt ctt tga 108
 Asn Cys Leu
 35

<210> 234
 <211> 35
 <212> PRT
 <213> Conus imperialis

<400> 234
 Ser Asp Gly Lys Ser Ala Ala Ala Lys Ala Lys Pro Ser His Leu Thr
 1 5 10 15

Ala Pro Phe Ile Arg Asp Glu Cys Cys Ser Asp Ser Arg Cys Gly Lys
 20 25 30

Asn Cys Leu
 35

<210> 235
 <211> 108
 <212> DNA
 <213> Conus imperialis

<220>
 <221> CDS
 <222> (1)...(105)

<400> 235
 ttt gat gga agg aat gcc cca gcc gac gac aaa gcg tct gac ctg atc 48
 Phe Asp Gly Arg Asn Ala Pro Ala Asp Asp Lys Ala Ser Asp Leu Ile
 1 5 10 15

gct caa atc gtc agg aga gca tgc tgt tcc gat cgt cgc tgt aga tgg 96
 Ala Gln Ile Val Arg Arg Ala Cys Cys Ser Asp Arg Arg Cys Arg Trp
 20 25 30

agg tgt ggt tga
 Arg Cys Gly
 35

<210> 236
 <211> 35
 <212> PRT
 <213> Conus imperialis

<400> 236
 Phe Asp Gly Arg Asn Ala Pro Ala Asp Asp Lys Ala Ser Asp Leu Ile
 1 5 10 15

Ala Gln Ile Val Arg Arg Ala Cys Cys Ser Asp Arg Arg Cys Arg Trp
 20 25 30

Arg Cys Gly
 35

<210> 237
 <211> 145
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)...(105)

<400> 237
 tct gat gga agg aat gcc gca gcc gac gcc aga gcg tct ccc cgg atc 48
 Ser Asp Gly Arg Asn Ala Ala Ala Asp Ala Arg Ala Ser Pro Arg Ile
 1 5 10 15

gct ctt ttc ctc agg ttc aca tgc tgt agg aga ggt acc tgg tcc cag 96
 Ala Leu Phe Leu Arg Phe Thr Cys Cys Arg Arg Gly Thr Cys Ser Gln
 20 25 30

cac tgt ggt tgaagacact gctgctccag gaccctctga accacgacgt 145
His Cys Gly
35

<210> 238
<211> 35
<212> PRT
<213> Conus regius

<400> 238
Ser Asp Gly Arg Asn Ala Ala Ala Asp Ala Arg Ala Ser Pro Arg Ile
1 5 10 15

Ala Leu Phe Leu Arg Phe Thr Cys Cys Arg Arg Gly Thr Cys Ser Gln
20 25 30

His Cys Gly
35

<210> 239
<211> 145
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(105)

<400> 239
tct aat gga agg aat gcc gca gcc gac gcc aaa gcg tct caa cg^g atc 48
Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile
1 5 10 15

gct cca ttc ctc agg gac tat tgc tgt agg aga cat gcc tgt acg ttg 96
Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg His Ala Cys Thr Leu
20 25 30

att tgt ggt tgaagacgct gctgctccag gaccctctga accacgacgt 145
Ile Cys Gly
35

<210> 240
<211> 35
<212> PRT
<213> Conus regius

<400> 240
Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile
1 5 10 15

Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg His Ala Cys Thr Leu
20 25 30

Ile Cys Gly
35

<210> 241
<211> 145
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(105)

<400> 241
tct aat gga agg aat gcc gca gcc gac gcc aaa gcg tct caa cgg atc 48
Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile
 1 5 10 15
gct cca ttc ctc agg gac tat tgc tgt agg aga cct ccc tgt acg ttg 96
Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg Pro Pro Cys Thr Leu
 20 25 30
att tgt ggt tgaagacgct gctgctccag gaccctctga accacgacgt 145
Ile Cys Gly
 35

<210> 242
<211> 35
<212> PRT
<213> Conus regius

<400> 242
Ser Asn Gly Arg Asn Ala Ala Ala Asp Ala Lys Ala Ser Gln Arg Ile 48
 1 5 10 15
Ala Pro Phe Leu Arg Asp Tyr Cys Cys Arg Arg Pro Pro Cys Thr Leu
 20 25 30
Ile Cys Gly
 35

<210> 243
<211> 136
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(96)

<400> 243
tct aat aaa agg aag aat gcc gca atg ctt gac atg atc gct caa cac 48
Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
 1 5 10 15
gcc ata agg ggt tgc tgt tcc gat cct cgc tgt aga tat aga tgt cgt 96
Ala Ile Arg Gly Cys Cys Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
 20 25 30

tgaagacgct gctgctccag gaccctctga accacgacgt 136

<210> 244
<211> 32
<212> PRT
<213> Conus regius

<400> 244
Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
 1 5 10 15

Ala Ile Arg Gly Cys Cys Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
 20 25 30

<210> 245
 <211> 145
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(105)

<400> 245
 ttt aat gga agg agt gcc gca gcc gac caa aat gcg cct ggc ctg atc 48
 Phe Asn Gly Arg Ser Ala Ala Ala Asp Gln Asn Ala Pro Gly Leu Ile
 1 5 10 15

gct caa gtc gtc aga gga ggg tgc tgt tcc gat ccc cgc tgc gcc tgg 96
 Ala Gln Val Val Arg Gly Gly Cys Cys Ser Asp Pro Arg Cys Ala Trp
 20 25 30

aga tgt ggt tgaagacgtt gctgctccag gaccctctga accacgacgt 145
 Arg Cys Gly
 35

<210> 246
 <211> 35
 <212> PRT
 <213> Conus regius

<400> 246
 Phe Asn Gly Arg Ser Ala Ala Ala Asp Gln Asn Ala Pro Gly Leu Ile
 1 5 10 15

Ala Gln Val Val Arg Gly Gly Cys Cys Ser Asp Pro Arg Cys Ala Trp
 20 25 30

Arg Cys Gly
 35

<210> 247
 <211> 145
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(105)

<400> 247
 ttt gat gga agg aat gcc gca gcc gac gcc aaa gtg att aac acg gtc 48
 Phe Asp Gly Arg Asn Ala Ala Ala Asp Ala Lys Val Ile Asn Thr Val
 1 5 10 15

gct cga atc gcc tgg gat ata tgc tgt tcc gaa cct gac tgt aac cat 96
 Ala Arg Ile Ala Trp Asp Ile Cys Cys Ser Glu Pro Asp Cys Asn His
 20 25 30

aaa tgt gtt tgaagacgtt tctgctccag gaccctctga accacgacgt 145
 Lys Cys Val
 35

<210> 248
<211> 35
<212> PRT
<213> Conus regius

<400> 248
Phe Asp Gly Arg Asn Ala Ala Ala Asp Ala Lys Val Ile Asn Thr Val
1 5 10 15
Ala Arg Ile Ala Trp Asp Ile Cys Cys Ser Glu Pro Asp Cys Asn His
20 25 30
Lys Cys Val
35

<210> 249
<211> 136
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)...(96)

<400> 249
tct aat aaa agg aag aat gcc gca atg ctt gac atg atc gct caa cac 48
Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
1 5 10 15
gcc ata agg ggt tgc tgt tcc gat cct cgc tgt aaa cat cag tgt ggt 96
Ala Ile Arg Gly Cys Cys Ser Asp Pro Arg Cys Lys His Gln Cys Gly
20 25 30
tgaagacgct gctgctccag gaccctctga accacgacgt 136

<210> 250
<211> 32
<212> PRT
<213> Conus regius

<400> 250
Ser Asn Lys Arg Lys Asn Ala Ala Met Leu Asp Met Ile Ala Gln His
1 5 10 15
Ala Ile Arg Gly Cys Cys Ser Asp Pro Arg Cys Lys His Gln Cys Gly
20 25 30

<210> 251
<211> 136
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)...(105)

<400> 251
atc aag aat aca gca gcc agc aac aaa gcg tct agc ctg gtg gct ctt 48
Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Ser Ser Leu Val Ala Leu
1 5 10 15

92

gtt gtc agg gga tgc tgt tac aat cct gtc tgc aag aaa tat tat tgt 96
Val Val Arg Gly Cys Cys Tyr Asn Pro Val Cys Lys Lys Tyr Tyr Cys
20 25 30

tgg aaa ggc tgatgctcca ggaccctctg aaccacgacg t 136
Trp Lys Gly
35

<210> 252
<211> 35
<212> PRT
<213> Conus musicus

<400> 252
Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Ser Ser Leu Val Ala Leu
1 5 10 15
Val Val Arg Gly Cys Cys Tyr Asn Pro Val Cys Lys Lys Tyr Tyr Cys
20 25 30
Trp Lys Gly
35

<210> 253
<211> 148
<212> DNA
<213> Conus purpurascens

<220>
<221> CDS
<222> (1)...(117)

<400> 253
tct gaa ggc agg aat gct gaa gcc atc gac aac gcc tta gac cag agg 48
Ser Glu Gly Arg Asn Ala Glu Ala Ile Asp Asn Ala Leu Asp Gln Arg
1 5 10 15

gat cca aag cga cag gag ccg ggg tgc tgt agg cat cct gcc tgt ggg 96
Asp Pro Lys Arg Gin Glu Pro Gly Cys Cys Arg His Pro Ala Cys Gly
20 25 30

aag aac aga tgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t 148
Lys Asn Arg Cys Gly Arg Arg
35

<210> 254
<211> 39
<212> PRT
<213> Conus purpurascens

<400> 254
Ser Glu Gly Arg Asn Ala Glu Ala Ile Asp Asn Ala Leu Asp Gln Arg
1 5 10 15
Asp Pro Lys Arg Gln Glu Pro Gly Cys Cys Arg His Pro Ala Cys Gly
20 25 30
Lys Asn Arg Cys Gly Arg Arg
35

<210> 255
<211> 156
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(102)

<400> 255
tct gat ggc agg aat att gca gtc gac gac aga tgg tct ttc tat acg 48
Ser Asp Gly Arg Asn Ile Ala Val Asp Asp Arg Trp Ser Phe Tyr Thr
1 5 10 15

ctc ttc cat gct act tgc tgt gcc gat cct gac tgt aga ttc cgg ccc 96
Leu Phe His Ala Thr Cys Cys Ala Asp Pro Asp Cys Arg Phe Arg Pro
20 25 30

ggg tgt tgatctttgt tcttcaaaga cgctgctggc ccaggaccct ctgaaccacg 152
Gly Cys

acgt 156

<210> 256
<211> 34
<212> PRT
<213> Conus musicus

<400> 256
Ser Asp Gly Arg Asn Ile Ala Val Asp Asp Arg Trp Ser Phe Tyr Thr 15
1 5 10 15

Leu Phe His Ala Thr Cys Cys Ala Asp Pro Asp Cys Arg Phe Arg Pro
20 25 30

Gly Cys

<210> 257
<211> 142
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(102)

<400> 257
atc aag aat act gca gcc agc aac aaa gcg cct agc ctg gtg gct att 48
Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Pro Ser Leu Val Ala Ile
1 5 10 15

gcc gtc agg gga tgc tgt tac aat cct tcc tgt tgg ccg aaa aca tat 96
Ala Val Arg Gly Cys Cys Tyr Asn Pro Ser Cys Trp Pro Lys Thr Tyr
20 25 30

tgt agt tggaaaggct gatgctccag gaccctctga accacgacgt 142
Cys Ser

<210> 258
<211> 34

<212> PRT
<213> Conus musicus

<400> 258
Ile Lys Asn Thr Ala Ala Ser Asn Lys Ala Pro Ser Leu Val Ala Ile
1 5 10 15
Ala Val Arg Gly Cys Cys Tyr Asn Pro Ser Cys Trp Pro Lys Thr Tyr
20 25 30
Cys Ser

<210> 259
<211> 161
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(108)

<400> 259
tct gat agc agg aat gtc gca atc gag gac aga gtg tct gac ctg cac 48
Ser Asp Ser Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu His
1 5 10 15
tct atg ttc ttc gat gtt tct tgc tgt agc aat cct acc tgt aaa gaa 96
Ser Met Phe Phe Asp Val Ser Cys Cys Ser Asn Pro Thr Cys Lys Glu
20 25 30
acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc 148
Thr Tyr Gly Cys
35
tgaaccacga cgt 161

<210> 260
<211> 36
<212> PRT
<213> Conus musicus

<400> 260
Ser Asp Ser Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu His
1 5 10 15
Ser Met Phe Phe Asp Val Ser Cys Cys Ser Asn Pro Thr Cys Lys Glu
20 25 30
Thr Tyr Gly Cys
35

<210> 261
<211> 156
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(102)

95

<400> 261
 tct gtt ggc agg aat att gca gtc gac gac aga ggg att ttc tct acg 48
 Ser Val Gly Arg Asn Ile Ala Val Asp Asp Arg Gly Ile Phe Ser Thr
 1 5 10 15

ctc ttc cat gct cat tgc tgt gcc aat ccc atc tgt aaa aac acg ccc 96
 Leu Phe His Ala His Cys Cys Ala Asn Pro Ile Cys Lys Asn Thr Pro
 20 25 30

ggt tgt tgatctttgt tcttcaaaga cgctgctggc ccaggaccct ctgaaccacg 152
 Gly Cys

acgt 156

<210> 262

<211> 34

<212> PRT

<213> Conus musicus

<400> 262

Ser Val Gly Arg Asn Ile Ala Val Asp Asp Arg Gly Ile Phe Ser Thr 48
 1 5 10 15

Leu Phe His Ala His Cys Cys Ala Asn Pro Ile Cys Lys Asn Thr Pro
 20 25 30

Gly Cys

<210> 263

<211> 161

<212> DNA

<213> Conus musicus

<220>

<221> CDS

<222> (1)...(108)

<400> 263

tcc gat ggc agg aat gtc gca atc gac gac aga gtg tct gac ctg cac 48
 Ser Asp Gly Arg Asn Val Ala Ile Asp Asp Arg Val Ser Asp Leu His
 1 5 10 15

tct atg ttc ttc gat att gct tgc tgt aac aat cct acc tgt aaa gaa 96
 Ser Met Phe Phe Asp Ile Ala Cys Cys Asn Asn Pro Thr Cys Lys Glu
 20 25 30

acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc 148
 Thr Tyr Gly Cys
 35

tgaaccacga cgt 161

<210> 264

<211> 36

<212> PRT

<213> Conus musicus

<400> 264

Ser Asp Gly Arg Asn Val Ala Ile Asp Asp Arg Val Ser Asp Leu His 48
 1 5 10 15

Ser Met Phe Phe Asp Ile Ala Cys Cys Asn Asn Pro Thr Cys Lys Glu
 20 25 30

Thr Tyr Gly Cys
 35

<210> 265
 <211> 161
 <212> DNA
 <213> Conus musicus

<220>
 <221> CDS
 <222> (1)..(108)

<400> 265
 tct gat ggc agg aat gtc gca atc gag gac aga gtg tct gac ctg ctc 48
 Ser Asp Gly Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu Leu
 1 5 10 15

tct atg ctc ttc gat gtt gct tgc tgt agc aat cct gtc tgt aaa gaa 96
 Ser Met Leu Phe Asp Val Ala Cys Cys Ser Asn Pro Val Cys Lys Glu
 20 25 30

acg tat ggt tgt tgatcggtgg ttttgaagac gctgatgctc caggaccctc 148
 Thr Tyr Gly Cys
 35

tgaaccacga cgt 161

<210> 266
 <211> 36
 <212> PRT
 <213> Conus musicus

<400> 266
 Ser Asp Gly Arg Asn Val Ala Ile Glu Asp Arg Val Ser Asp Leu Leu
 1 5 10 15

Ser Met Leu Phe Asp Val Ala Cys Cys Ser Asn Pro Val Cys Lys Glu
 20 25 30

Thr Tyr Gly Cys
 35

<210> 267
 <211> 154
 <212> DNA
 <213> Conus betulinus

<220>
 <221> CDS
 <222> (1)..(123)

<400> 267
 tat gat ggc agg aat gct gcc gcc gac gac aaa gct ttt gac ctg ctg 48
 Tyr Asp Gly Arg Asn Ala Ala Ala Asp Asp Lys Ala Phe Asp Leu Leu
 1 5 10 15

gct atg acc ata agg gga gga tgc tgt tcc tat cct ccc tgt atc gcg 96
 Ala Met Thr Ile Arg Gly Gly Cys Cys Ser Tyr Pro Pro Cys Ile Ala

97

20

25

30

agt aat cct aaa tgt ggt gga aga cgc ttagtgcctcca ggaccctctg 143
Ser Asn Pro Lys Cys Gly Gly Arg Arg
35 40

aaccacaacg t 154

<210> 268
<211> 41
<212> PRT
<213> Conus betulinus

<400> 268
Tyr Asp Gly Arg Asn Ala Ala Ala Asp Asp Lys Ala Phe Asp Leu Leu
1 5 10 15

Ala Met Thr Ile Arg Gly Gly Cys Cys Ser Tyr Pro Pro Cys Ile Ala
20 25 30

Ser Asn Pro Lys Cys Gly Gly Arg Arg
35 40

<210> 269
<211> 151
<212> DNA
<213> Conus lividus

<220>
<221> CDS
<222> (1)..(111)

<400> 269
ttt gat ggc agg aat gct gca ggc aac gcc aaa atg tcc gcc ctg atg 48
Phe Asp Gly Arg Asn Ala Ala Gly Asn Ala Lys Met Ser Ala Leu Met
1 5 10 15

gcc ctg acc atc agg gga tgc tgt tcc cat cct gtc tgt agc gcg atg 96
Ala Leu Thr Ile Arg Gly Cys Cys Ser His Pro Val Cys Ser Ala Met
20 25 30

agt cca atc tgt ggc tgaagacgct gatgccccag gaccctctga accacgacgt 151
Ser Pro Ile Cys Gly
35

<210> 270
<211> 37
<212> PRT
<213> Conus lividus

<400> 270
Phe Asp Gly Arg Asn Ala Ala Gly Asn Ala Lys Met Ser Ala Leu Met
1 5 10 15

Ala Leu Thr Ile Arg Gly Cys Cys Ser His Pro Val Cys Ser Ala Met
20 25 30

Ser Pro Ile Cys Gly
35

<210> 271
<211> 196
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(165)

<400> 271
atc aag aat gct gca gct gac gac aaa gca tct gac ctg ctc tct cag 48
Ile Lys Asn Ala Ala Ala Asp Asp Lys Ala Ser Asp Leu Leu Ser Gln
1 5 10 15

atc gtc agg aat gct gca tcc aat gac aaa ggg tct gac ctg atg act 96
Ile Val Arg Asn Ala Ala Ser Asn Asp Lys Gly Ser Asp Leu Met Thr
20 25 30

ctt gcc ctc agg gga tgc tgt aaa aat cct tac tgt ggt gcg tcg aaa 144
Leu Ala Leu Arg Gly Cys Cys Lys Asn Pro Tyr Cys Gly Ala Ser Lys
35 40 45

aca tat tgt ggt aga aga cgc tgatgctcca ggaccctctg aaccacgacg t 196
Thr Tyr Cys Gly Arg Arg Arg
50 55

<210> 272
<211> 55
<212> PRT
<213> Conus musicus

<400> 272
Ile Lys Asn Ala Ala Ala Asp Asp Lys Ala Ser Asp Leu Leu Ser Gln
1 5 10 15

Ile Val Arg Asn Ala Ala Ser Asn Asp Lys Gly Ser Asp Leu Met Thr
20 25 30

Leu Ala Leu Arg Gly Cys Cys Lys Asn Pro Tyr Cys Gly Ala Ser Lys
35 40 45

Thr Tyr Cys Gly Arg Arg Arg
50 55

<210> 273
<211> 139
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (40)..(108)

<400> 273
tctgatggca ggaatgccgc agcgtctgac ctgatggat ctg acc atc aag gga 54
Leu Thr Ile Lys Gly
1 5

tgc tgt tct tat cct ccc tgt ttc gcg act aat cca gac tgt ggt cga 102
Cys Cys Ser Tyr Pro Pro Cys Phe Ala Thr Asn Pro Asp Cys Gly Arg
10 15 20

cga cgc ttagtgcctcca ggaccctctg aaccacgacg t 139
 Arg Arg

<210> 274

<211> 23

<212> PRT

<213> Conus omaria

<400> 274

Leu	Thr	Ile	Lys	Gly	Cys	Cys	Ser	Tyr	Pro	Pro	Cys	Phe	Ala	Thr	Asn
1				5				10					15		

Pro	Asp	Cys	Gly	Arg	Arg	Arg
			20			

<210> 275

<211> 126

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (1)...(123)

<400> 275

ttt	aat	ggc	agg	aat	gcc	gca	gcc	gac	tac	aaa	ggg	tct	gaa	ttg	ctc
Phe	Asp	Gly	Arg	Asn	Ala	Ala	Ala	Asp	Tyr	Lys	Gly	Ser	Glu	Leu	Leu
1				5					10				15		

gct	atg	acc	gtc	agg	gga	gga	tgc	tgt	tcc	tat	cct	ccc	tgt	atc	gca
Ala	Met	Thr	Val	Arg	Gly	Gly	Cys	Cys	Ser	Tyr	Pro	Pro	Cys	Ile	Ala
			20					25					30		

aat	aat	cct	ctt	tgt	gct	gga	aga	cgc	tga						126
Asn	Asn	Pro	Leu	Cys	Ala	Gly	Arg	Arg							
			35				40								

<210> 276

<211> 41

<212> PRT

<213> Conus radiatus

<400> 276

Phe	Asp	Gly	Arg	Asn	Ala	Ala	Ala	Asp	Tyr	Lys	Gly	Ser	Glu	Leu	Leu
1				5					10				15		

Ala	Met	Thr	Val	Arg	Gly	Gly	Cys	Cys	Ser	Tyr	Pro	Pro	Cys	Ile	Ala
			20				25						30		

Asn	Asn	Pro	Leu	Cys	Ala	Gly	Arg	Arg							
			35				40								

<210> 277

<211> 126

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (1)...(123)

100

<400> 277
 ttt gat ggc agg aat gcc gca gcc gac tac aaa ggg tct gaa ttg ctc 48
 Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr Lys Gly Ser Glu Leu Leu
 1 5 10 15

gct atg acc gtc agg gga gga tgc tgt tcc tat cct ccc tgt atc gca 96
 Ala Met Thr Val Arg Gly Gly Cys Cys Ser Tyr Pro Pro Cys Ile Ala
 20 25 30

aat aat cct ttt tgt gct gga aga cgc tga 126
 Asn Asn Pro Phe Cys Ala Gly Arg Arg
 35 40

<210> 278
<211> 41
<212> PRT
<213> Conus radiatus

<400> 278
 Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr Lys Gly Ser Glu Leu Leu
 1 5 10 15

Ala Met Thr Val Arg Gly Gly Cys Cys Ser Tyr Pro Pro Cys Ile Ala
 20 25 30

Asn Asn Pro Phe Cys Ala Gly Arg Arg
 35 40

<210> 279
<211> 155
<212> DNA
<213> Conus virgo

<220>
<221> CDS
<222> (1)..(114)

<400> 279
 tct tat gac agg tat gcc tcg ccc gtc gac aga gcg tct gcc ctg atc 48
 Ser Tyr Asp Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
 1 5 10 15

gct cag gcc atc ctt cga gat tgc tgt tcc aat cct ccc tgt tcc caa 96
 Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ser Gln
 20 25 30

aat aat cca gac tgt atg taaagacgct gcttgctcca ggaccctctg 144
 Asn Asn Pro Asp Cys Met
 35

aaccacgacg t 155

<210> 280
<211> 38
<212> PRT
<213> Conus virgo

<400> 280
 Ser Tyr Asp Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
 1 5 10 15

101

Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ser Gln
 20 25 30

 Asn Asn Pro Asp Cys Met
 35

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<210> 281
<211> 155
<212> DNA
<213> Conus virgo

<220>
<221> CDS
<222> (1)..(114)

<400> 281
tct tat ggc agg tat gcc tca ccc gtc gac aga gcg tct gcc ctg atc 48
Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
 1           5           10          15

gct cag gcc atc ctt cga gat tgc tgc tcc aat cct cct tgt gcc cat 96
Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ala His
 20          25          30

aat aat cca gac tgt cgt taaagacgct gcttgctcca ggaccctctg 14
Asn Asn Pro Asp Cys Arg
 35

aaccacqacq t

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<210> 282
<211> 38
<212> PRT
<213> Conus virgo

<400> 282
Ser Tyr Gly Arg Tyr Ala Ser Pro Val Asp Arg Ala Ser Ala Leu Ile
      1           5           10          15

Ala Gln Ala Ile Leu Arg Asp Cys Cys Ser Asn Pro Pro Cys Ala His
      20          25          30

Asn Asn Pro Asp Cys Arg
      35

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<210> 283
<211> 126
<212> DNA
<213> Conus achatinus

<220>
<221> CDS
<222> (1)...(123)

<400> 283
tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct ggc atg agc 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Gly Met Ser
   1           5           10          15

gcg ctg gcc gtc aat gaa tgc tgt acc aac cct gtc tgt cac gcg gaa 96
Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Ala Glu

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102

20

25

30

cat caa gaa ctt tgt gct aga aga cgc tga 126
His Gln Glu Leu Cys Ala Arg Arg Arg
35 40

<210> 284
<211> 41
<212> PRT
<213> Conus achatinus

<400> 284
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Gly Met Ser
1 5 10 15

Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Ala Glu
20 25 30

His Gln Glu Leu Cys Ala Arg Arg Arg
35 40

<210> 285
<211> 126
<212> DNA
<213> *Conus achatinus*

<220>
<221> CDS
<222> (1)..(123)

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<400> 285
tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct gac gtg atc 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Asp Val Ile
   1           5           10          15

```

acg ctg gcc ctc aag gga tgc tgt tcc aac cct gtc tgt cac ttg gag 96
 Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn Pro Val Cys His Leu Glu
 20 25 30

cat tca aac ctt tgt ggt aga aga aga cgc tga 126
His Ser Asn Leu Cys Gly Arg Arg Arg
 35 40

<210> 286
<211> 41
<212> PRT
<213> Conus achatinus

<400> 286
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Asp Val Ile
1 5 10 15

Thr Leu Ala Leu Lys Gly Cys Cys Ser Asn Pro Val Cys His Leu Glu
20 25 30

His Ser Asn Leu Cys Gly Arg Arg Arg
35 40

<210> 287
<211> 126

<212> DNA
<213> Conus achatinus

<220>
<221> CDS
<222> (1)..(123)

<400> 287
tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct ggc atg agc 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Gly Met Ser
1 5 10 15

gcg ctg gcc gtc aat gaa tgc tgt acc aac cct gtc tgt cac gtg gaa 96
Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Val Glu
20 25 30

cat caa gaa ctt tgt gct aga aga cgc tga 126
His Gln Glu Leu Cys Ala Arg Arg Arg
35 40

<210> 288
<211> 41
<212> PRT
<213> Conus achatinus

<400> 288
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Gly Met Ser 15
1 5 10

Ala Leu Ala Val Asn Glu Cys Cys Thr Asn Pro Val Cys His Val Glu
20 25 30

His Gln Glu Leu Cys Ala Arg Arg Arg
35 40

<210> 289
<211> 220
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(180)

<400> 289
atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca gat cgt gca ttt cgt ggc agg aat gcc gca gcc aaa gcg 96
Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Ala Lys Ala
20 25 30

tct ggc ctg gtc ggt ctg acc gac aag agg caa gaa tgc tgt tct tat 144
Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Glu Cys Cys Ser Tyr
35 40 45

cct gcc tgt aac cta gat cat cca gaa ctt tgt ggt tgaagacgct 190
Pro Ala Cys Asn Leu Asp His Pro Glu Leu Cys Gly
50 55 60

gatgctccag gaccctctga accacgacgt 220

<210> 290
<211> 60
<212> PRT
<213> Conus ammiralis

<400> 290
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Phe Thr Ser Asp Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys Ala
20 25 30
Ser Gly Leu Val Gly Leu Thr Asp Lys Arg Gln Glu Cys Cys Ser Tyr
35 40 45
Pro Ala Cys Asn Leu Asp His Pro Glu Leu Cys Gly
50 55 60

<210> 291
<211> 223
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(192)

<400> 291
atg ttc acc gtc ttt ctg ttg gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
tcc act tca ggt cgt cgt gca ttt cgt ggc agg aat gcc gca gcc aaa 96
Ser Thr Ser Gly Arg Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys
20 25 30
gcg tct gga ctg gtc ggt ctg act gac agg aga cca gaa tgc tgt agt 144
Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
35 40 45
gat cct cgc tgt aac tcg act cat cca gaa ctt tgt ggt gga aga cgc 192
Asp Pro Arg Cys Asn Ser Thr His Pro Glu Leu Cys Gly Gly Arg Arg
50 55 60
tgatgctcca ggaccctctg aaccacgacg t 223

<210> 292
<211> 64
<212> PRT
<213> Conus ammiralis

<400> 292
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Ser Thr Ser Gly Arg Arg Ala Phe Arg Gly Arg Asn Ala Ala Lys
20 25 30
Ala Ser Gly Leu Val Gly Leu Thr Asp Arg Arg Pro Glu Cys Cys Ser
35 40 45

105

Asp Pro Arg Cys Asn Ser Thr His Pro Glu Leu Cys Gly Gly Arg Arg
 50 55 60

<210> 293
<211> 151
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (1)..(120)

<400> 293
tct gat ggc agg aat gcc gca gcc aac gcg ttt gac ctg atc gat ctg 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Phe Asp Leu Ile Asp Leu
 1 5 10 15

acc gcc agg cta aat tgc tgt atg att ccc ccc tgt tgg aag aaa tat 96
Thr Ala Arg Leu Asn Cys Cys Met Ile Pro Pro Cys Trp Lys Lys Tyr
 20 25 30

gga gac aga tgt agt gaa gta cgc tgatgctcca ggaccctctg aaccacgacg 150
Gly Asp Arg Cys Ser Glu Val Arg
 35 40

t 151

<210> 294
<211> 40
<212> PRT
<213> Conus arenatus

<400> 294
Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Phe Asp Leu Ile Asp Leu
 1 5 10 15

Thr Ala Arg Leu Asn Cys Cys Met Ile Pro Pro Cys Trp Lys Lys Tyr
 20 25 30

Gly Asp Arg Cys Ser Glu Val Arg
 35 40

<210> 295
<211> 126
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (1)..(93)

<400> 295
tct gat ggc agg aat gcc gca cgc aaa gcg ttt ggc tgc tgc gac tta 48
Ser Asp Gly Arg Asn Ala Ala Arg Lys Ala Phe Gly Cys Cys Asp Leu
 1 5 10 15

ata ccc tgt ttg gag aga tat ggt aac aga tgt aat gaa gtg cac 93
Ile Pro Cys Leu Glu Arg Tyr Gly Asn Arg Cys Asn Glu Val His
 20 25 30

tgatgctcca ggaccctctg aaccacgacg cgt 126

<210> 296
<211> 31
<212> PRT
<213> Conus arenatus

<400> 296
Ser Asp Gly Arg Asn Ala Ala Arg Lys Ala Phe Gly Cys Cys Asp Leu
1 5 10 15

Ile Pro Cys Leu Glu Arg Tyr Gly Asn Arg Cys Asn Glu Val His
20 25 30

<210> 297
<211> 151
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (1)...(120)

<400> 297
tct gat ggc agc aat gcc gca gcc aac gag ttt gac ctg atc gct ctg 48
Ser Asp Gly Ser Asn Ala Ala Asn Glu Phe Asp Leu Ile Ala Leu
1 5 10 15

acc gcc agg cta ggt tgc tgt aac gtt aca ccc tgt tgg gag aaa tat 96
Thr Ala Arg Leu Gly Cys Cys Asn Val Thr Pro Cys Trp Glu Lys Tyr
20 25 30

gga gac aaa tgt aat gaa gta cgc tgatgcttca ggaccctctg aaccacgacg 150
Gly Asp Lys Cys Asn Glu Val Arg
35 40

t 151

<210> 298
<211> 40
<212> PRT
<213> Conus arenatus

<400> 298
Ser Asp Gly Ser Asn Ala Ala Asn Glu Phe Asp Leu Ile Ala Leu
1 5 10 15

Thr Ala Arg Leu Gly Cys Cys Asn Val Thr Pro Cys Trp Glu Lys Tyr
20 25 30

Gly Asp Lys Cys Asn Glu Val Arg
35 40

<210> 299
<211> 148
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (1)...(117)

107

<400> 299
tct gat ggc agg aat gtc gca gca aaa gcg ttt cac cgg atc ggc cgg 48
Ser Asp Gly Arg Asn Val Ala Ala Lys Ala Phe His Arg Ile Gly Arg
1 5 10 15

acc atc agg gat gaa tgc tgt tcc aat cct gcc tgt agg gtg aat aat 96
Thr Ile Arg Asp Glu Cys Cys Ser Asn Pro Ala Cys Arg Val Asn Asn
20 25 30

cca cac gtt tgt aga cga cgc tgatgctcca ggaccctctg aaccacgacg t 148
Pro His Val Cys Arg Arg Arg
35

<210> 300

<211> 39

<212> PRT

<213> Conus arenatus

<400> 300
Ser Asp Gly Arg Asn Val Ala Ala Lys Ala Phe His Arg Ile Gly Arg
1 5 10 15

Thr Ile Arg Asp Glu Cys Cys Ser Asn Pro Ala Cys Arg Val Asn Asn
20 25 30

Pro His Val Cys Arg Arg Arg
35

<210> 301

<211> 151

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (1)..(120)

<400> 301
tct gat ggc agg aat gcc gca gcc aac gcg ttt gac ctg atg cct ctg 48
Ser Asp Gly Arg Asn Ala Ala Asn Ala Phe Asp Leu Met Pro Leu
1 5 10 15

acc gcc agg cta aat tgc tgt agc att ccc ggc tgt tgg aac gaa tat 96
Thr Ala Arg Leu Asn Cys Cys Ser Ile Pro Gly Cys Trp Asn Glu Tyr
20 25 30

aaa gac aga tgt agt aaa gta cgc tgatgctcca ggaccctctg aaccacgacg 150
Lys Asp Arg Cys Ser Lys Val Arg
35 40

t 151

<210> 302

<211> 40

<212> PRT

<213> Conus arenatus

<400> 302
Ser Asp Gly Arg Asn Ala Ala Asn Ala Phe Asp Leu Met Pro Leu
1 5 10 15

108

Thr Ala Arg Leu Asn Cys Cys Ser Ile Pro Gly Cys Trp Asn Glu Tyr
20 25 30

Lys Asp Arg Cys Ser Lys Val Arg
35 40

<210> 303
<211> 157
<212> DNA
<213> Conus aurisiacus

<220>
<221> CDS
<222> (52)..(126)

<400> 303
tctgatggca ggaatgccgc agccgacgac aaagcgtctg acctggtcgc t ctg gtc 57
Leu Val
1

gtc agg gga gga tgc tgt tcc cac cct gtc tgt tac ttt aat aat cca 105
Val Arg Gly Gly Cys Cys Ser His Pro Val Cys Tyr Phe Asn Asn Pro
5 10 15

caa atg tgt cgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t 157
Gln Met Cys Arg Gly Arg Arg
20 25

<210> 304
<211> 25
<212> PRT
<213> Conus aurisiacus

<400> 304
Leu Val Val Arg Gly Gly Cys Cys Ser His Pro Val Cys Tyr Phe Asn
1 5 10 15

Asn Pro Gln Met Cys Arg Gly Arg Arg
20 25

<210> 305
<211> 157
<212> DNA
<213> Conus aurisiacus

<220>
<221> CDS
<222> (52)..(126)

<400> 305
tctgatggca ggaatgccgc agccgacgac aaagcgtctg acctggtcgc t ctg gcc 57
Leu Ala
1

gtc agg gga gga tgc tgt tcc cac cct gtc tgt aac ttg aat aat cca 105
Val Arg Gly Gly Cys Cys Ser His Pro Val Cys Asn Leu Asn Asn Pro
5 10 15

caa atg tgt cgt gga aga cgc tgatgctcca ggaccctctg aaccacgacg t 157
Gln Met Cys Arg Gly Arg Arg
20 25

<210> 306
<211> 25
<212> PRT
<213> Conus aurisiacus

<400> 306
Leu Ala Val Arg Gly Gly Cys Cys Ser His Pro Val Cys Asn Leu Asn
1 5 10 15
Asn Pro Gln Met Cys Arg Gly Arg Arg
20 25

<210> 307
<211> 157
<212> DNA
<213> Conus betulinus

<220>
<221> CDS
<222> (1)...(117)

<400> 307
ttt cgt ggc agg aat ccc gca gcc aac gac aaa agg tct gac ctg gcc 48
Phe Arg Gly Arg Asn Pro Ala Ala Asn Asp Lys Arg Ser Asp Leu Ala
1 5 10 15

^ gct ctg agc gtc agg gga gga tgc tgt tcc cat cct gcc tgt agc gtg 96
Ala Leu Ser Val Arg Gly Gly Cys Cys Ser His Pro Ala Cys Ser Val
20 25 30

act cat cca gag ctt tgt ggc tgaagacgct gatgccccag gaccctctga 147
Thr His Pro Glu Leu Cys Gly
35

accacgacgt 157

<210> 308
<211> 39
<212> PRT
<213> Conus betulinus

<400> 308
Phe Arg Gly Arg Asn Pro Ala Ala Asn Asp Lys Arg Ser Asp Leu Ala
1 5 10 15
Ala Leu Ser Val Arg Gly Gly Cys Cys Ser His Pro Ala Cys Ser Val
20 25 30
Thr His Pro Glu Leu Cys Gly

<210> 309
<211> 151
<212> DNA
<213> Conus betulinus

<220>
<221> CDS
<222> (1)...(120)

110

<400> 309
tct gat ggc ggg aat gcc gca gcc aaa gcg tct gac ctg atc gct cag 48
Ser Asp Gly Gly Asn Ala Ala Ala Lys Ala Ser Asp Leu Ile Ala Gln
1 5 10 15

acc atc agg gga gga tgc tgt tcc tat cct gcc tgt agc gtg gaa cat 96
Thr Ile Arg Gly Gly Cys Cys Ser Tyr Pro Ala Cys Ser Val Glu His
20 25 30

caa gac ctt tgt gat gga aga cgc tgatgctcca ggaccctctg aaccacgacg 150
Gln Asp Leu Cys Asp Gly Arg Arg
35 40

t 151

<210> 310
<211> 40
<212> PRT
<213> Conus betulinus

<400> 310
Ser Asp Gly Gly Asn Ala Ala Ala Lys Ala Ser Asp Leu Ile Ala Gln 48
1 5 10 15

Thr Ile Arg Gly Gly Cys Cys Ser Tyr Pro Ala Cys Ser Val Glu His
20 25 30

Gln Asp Leu Cys Asp Gly Arg Arg
35 40

<210> 311
<211> 114
<212> DNA
<213> Conus characteristicus

<220>
<221> CDS
<222> (1)...(111)

<400> 311
tct tat ggc agg aat gcc gca gcc aaa gcg ttt gaa gtg agt tgc tgt 48
Ser Tyr Gly Arg Asn Ala Ala Ala Lys Ala Phe Glu Val Ser Cys Cys
1 5 10 15

gtc gtt cgc ccc tgt tgg att cgc tat caa gag gaa tgt ctt gaa gca 96
Val Val Arg Pro Cys Trp Ile Arg Tyr Gln Glu Glu Cys Leu Glu Ala
20 25 30

gat ccc agg acc ctc tga 114
Asp Pro Arg Thr Leu
35

<210> 312
<211> 37
<212> PRT
<213> Conus characteristicus

<400> 312
Ser Tyr Gly Arg Asn Ala Ala Ala Lys Ala Phe Glu Val Ser Cys Cys
1 5 10 15

111

Val Val Arg Pro Cys Trp Ile Arg Tyr Gln Glu Glu Cys Leu Glu Ala
20 25 30

Asp Pro Arg Thr Leu
35

<210> 313
<211> 123
<212> DNA
<213> Conus characteristicus

<220>
<221> CDS
<222> (1)..(120)

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<400> 313
tct gat ggc agg aat gcc gca gcc aac gcc ctt gac ctg atc act ctg 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Leu Asp Leu Ile Thr Leu
   1           5           10          15

```

atc gcc agg caa aat tgc tgt agc att ccc ggc tgt tgg gag aaa tat 96
 Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro Gly Cys Trp Glu Lys Tyr
 20 25 30

gga gac aaa tgt agt gaa gta cgc tga 123
 Gly Asp Lys Cys Ser Glu Val Arg
 35 40

<210> 314
<211> 40
<212> PRT
<213> *Conus characteristicus*

<400> 314
Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala Leu Asp Leu Ile Thr Leu
1 5 10 15

Ile Ala Arg Gln Asn Cys Cys Ser Ile Pro Gly Cys Trp Glu Lys Tyr
20 25 30

Gly Asp Lys Cys Ser Glu Val Arg
35 40

<210> 315
<211> 154
<212> DNA
<213> *Conus catus*

<220>
<221> CDS
<222> (1) .. (123)

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<400> 315
tct gat ggc agg aat gaa gca gcc aac gac gaa gcg tct gac gtg atc 48
Ser Asp Gly Arg Asn Glu Ala Ala Asn Asp Glu Ala Ser Asp Val Ile
          1           5           10          15

```

gag ctg gcc ctc aag gga tgc tgt tcc aac cct gtc tgt cac ttg gag 96
 Glu Leu Ala Leu Lys Gly Cys Cys Ser Asn Pro Val Cys His Leu Glu
 20 25 30

112

cat cca aac gct tgt ggt aga aga cgc tgatgctcca ggaccctctg 143
His Pro Asn Ala Cys Gly Arg Arg Arg
35 40

aaccacgacq t 154

<210> 316
<211> 41
<212> PRT
<213> Conus catus

<400> 316
Ser Asp Gly Arg Asn Glu Ala Ala Asn Asp Glu Ala Ser Asp Val Ile
1 5 10 15

Glu Leu Ala Leu Lys Gly Cys Cys Ser Asn Pro Val Cys His Leu Glu
20 25 30

His Pro Asn Ala Cys Gly Arg Arg Arg
35 40

<210> 317
<211> 154
<212> DNA
<213> *Conus catus*

<220>
<221> CDS
<222> (1) .. (123)

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<400> 317
tct gat ggc agg aat gcc gca gcc aac gac aaa gcg tct gac ctg gtc 48
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Asp Leu Val
   1       5       10      15

```

gct ctg gcc gtc agg gga tgc tgt tcc aac cct atc tgt tac ttt aat 96
Ala Leu Ala Val Arg Gly Cys Cys Ser Asn Pro Ile Cys Tyr Phe Asn
20 25 30

aat cca cga att tgt cgt gga aga cgc tgatgctcca ggaccctctg 143
Asn Pro Arg Ile Cys Arg Gly Arg Arg
35 40

зассасасаса т 154

<210> 318
<211> 41
<212> PRT
<213> *Corpus catus*

<400> 318
Ser Asp Gly Arg Asn Ala Ala Ala Asn Asp Lys Ala Ser Asp Leu Val
1 5 10 15

Ala Leu Ala Val Arg Gly Cys Cys Ser Asn Pro Ile Cys Tyr Phe Asn
20 25 30

Asn Pro Arg Ile Cys Arg Gly Arg Arg
35 40

<210> 319
<211> 111
<212> DNA
<213> Conus episcopatus

<220>
<221> CDS
<222> (1)..(108)

<400> 319
tct cat ggc agg aat gcc gca cgc aaa gcg tct gac ctg atc gct ctg 48
Ser His Gly Arg Asn Ala Ala Arg Lys Ala Ser Asp Leu Ile Ala Leu
 1 5 10 15
acc gtc agg gaa tgc tgt tct cag cct ccc tgt cgc tgg aaa cat cca 96
Thr Val Arg Glu Cys Cys Ser Gln Pro Pro Cys Arg Trp Lys His Pro
 20 25 30
gaa ctt tgt agt tga 111
Glu Leu Cys Ser
 35

<210> 320
<211> 36
<212> PRT
<213> Conus episcopatus

<400> 320
Ser His Gly Arg Asn Ala Ala Arg Lys Ala Ser Asp Leu Ile Ala Leu
 1 5 10 15
Thr Val Arg Glu Cys Cys Ser Gln Pro Pro Cys Arg Trp Lys His Pro
 20 25 30
Glu Leu Cys Ser
 35

<210> 321
<211> 151
<212> DNA
<213> Conus geographus

<220>
<221> CDS
<222> (1)..(120)

<400> 321
tct gat ggc agg aat gac gca gcc aaa gcg ttt gac ctg ata tct tcg 48
Ser Asp Gly Arg Asn Asp Ala Ala Lys Ala Phe Asp Leu Ile Ser Ser
 1 5 10 15
acc gtc aag aaa gga tgc tgt tcc cat cct gcc tgt gcg ggg aat aat 96
Thr Val Lys Lys Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn Asn
 20 25 30
caa cat att tgt ggc cga aga cgc tgatgctcca ggaccctctg aaccacgacg 150
Gln His Ile Cys Gly Arg Arg Arg
 35 40

<210> 322

<211> 40

<212> PRT

<213> Conus geographus

<400> 322

Ser	Asp	Gly	Arg	Asn	Asp	Ala	Ala	Lys	Ala	Phe	Asp	Leu	Ile	Ser	Ser
1				5					10				15		

Thr	Val	Lys	Lys	Gly	Cys	Cys	Ser	His	Pro	Ala	Cys	Ala	Gly	Asn	Asn
		20					25					30			

Gln	His	Ile	Cys	Gly	Arg	Arg	Arg
		35			40		

<210> 323

<211> 154

<212> DNA

<213> Conus geographus

<220>

<221> CDS

<222> (1)..(123)

<400> 323

tct	gat	ggc	agg	aat	gcc	gca	gcc	aac	gac	caa	gcg	tct	gac	ctg	atg	48
Ser	Asp	Gly	Arg	Asn	Ala	Ala	Ala	Asn	Asp	Gln	Ala	Ser	Asp	Leu	Met	
1				5					10				15			

gct	gcg	acc	gtc	agg	gga	tgc	tgt	gcc	gtt	cct	tcc	tgt	cgc	ctc	cgt	96
Ala	Ala	Thr	Val	Arg	Gly	Cys	Cys	Ala	Val	Pro	Ser	Cys	Arg	Leu	Arg	
		20					25					30				

aat	cca	gac	ctt	tgt	ggt	gga	gga	cgc	tgtatgc	ccca	ggaccctctg		143
Asn	Pro	Asp	Leu	Cys	Gly	Gly	Gly	Arg					
	35					40							

aaccacgacg	t		154
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<210> 324

<211> 41

<212> PRT

<213> Conus geographus

<400> 324

Ser	Asp	Gly	Arg	Asn	Ala	Ala	Ala	Asn	Asp	Gln	Ala	Ser	Asp	Leu	Met
1				5					10				15		

Ala	Ala	Thr	Val	Arg	Gly	Cys	Cys	Ala	Val	Pro	Ser	Cys	Arg	Leu	Arg
		20					25					30			

Asn	Pro	Asp	Leu	Cys	Gly	Gly	Gly	Arg
	35				40			

<210> 325

<211> 120

<212> DNA

<213> Conus imperialis

<220>

<221> CDS

115

<222> (1)..(117)

<400> 325
 ctt gat gaa agg aat gcc gca gcc gac gac aaa gcg tct gac ctg atc 48
 Leu Asp Glu Arg Asn Ala Ala Ala Asp Asp Lys Ala Ser Asp Leu Ile
 1 5 . 10 15

gct caa atc gtc agg aga gga tgc tgt tcc cat cct gcc tgt aac gtg 96
 Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Ala Cys Asn Val
 20 25 30

aat aat cca cac att tgt ggt tga 120
 Asn Asn Pro His Ile Cys Gly
 35

<210> 326

<211> 39

<212> PRT

<213> Conus imperialis

<400> 326
 Leu Asp Glu Arg Asn Ala Ala Ala Asp Asp Lys Ala Ser Asp Leu Ile 48
 1 5 10 15

Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Ala Cys Asn Val
 20 25 30

Asn Asn Pro His Ile Cys Gly
 35

<210> 327

<211> 142

<212> DNA

<213> Conus lividus

<220>

<221> CDS

<222> (1)..(111)

<400> 327
 tct gat ggc agg aat act gca gcc aaa gtc aaa tat tct aag acg ccg 48
 Ser Asp Gly Arg Asn Thr Ala Ala Lys Val Lys Tyr Ser Lys Thr Pro
 1 5 10 15

gag gaa tgc tgt ccc aat cct ccc tgt ttc gcg aca aat tcg gat att 96
 Glu Glu Cys Cys Pro Asn Pro Pro Cys Phe Ala Thr Asn Ser Asp Ile
 20 25 30

tgt ggc gga aga cgc tgatgctcca ggaccctctg aaccacgacg t 142
 Cys Gly Gly Arg Arg
 35

<210> 328

<211> 37

<212> PRT

<213> Conus lividus

<400> 328
 Ser Asp Gly Arg Asn Thr Ala Ala Lys Val Lys Tyr Ser Lys Thr Pro 48
 1 5 10 15

Glu Glu Cys Cys Pro Asn Pro Pro Cys Phe Ala Thr Asn Ser Asp Ile
20 25 30

Cys Gly Gly Arg Arg
35

<210> 329
<211> 157
<212> DNA
<213> *Conus lividus*

<220>
<221> CDS
<222> (1)..(117)

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<400> 329
tctaatggcaggaatgccgcagccaaattcaaagcgcctgccctgtatg 48
Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
1 5 10 15

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aag cg acc gtc agg gat gct tgc tgt tca gac cct cgc tgt tcc ggg 96
Lys Arg Thr Val Arg Asp Ala Cys Cys Ser Asp Pro Arg Cys Ser Gly
20 25 30

aaa cat caa gac ctg tgt ggc tgaagacgct gatgctccag gaccctctga 147
Lys His Gln Asp Leu Cys Gly
35

accacgacgt 157

<210> 330
<211> 39
<212> PRT
<213> *Corus lividus*

<400> 330
Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
1 5 10 15

Lys Arg Thr Val Arg Asp Ala Cys Cys Ser Asp Pro Arg Cys Ser Gly
20 25 30

Lys His Gln Asp Leu Cys Gly
35

<210> 331
<211> 157
<212> DNA
<213> *Conus lividus*

<220>
<221> CDS
<222> (1)..(117)

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<400> 331
tctaatggcaggatatgccgcagccaaaatcgtttccaaagcgccctgccctgtatg 48
Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
1           5           ,           10          15

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gag ctg acc gtc agg gaa gat tgc tgt tca gac cct cgc tgt tcc gtg 96
 Glu Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val

117

20

25

30

gga cat caa gac ctg tgt ggc tgaagacgct gatgctccag gaccctctga 147
 Gly His Gln Asp Leu Cys Gly
 35

accacgacgt 157

<210> 332

<211> 39

<212> PRT

<213> Conus lividus

<400> 332

Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
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Glu Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val
 20 25 30

Gly His Gln Asp Leu Cys Gly
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<210> 333

<211> 157

<212> DNA

<213> Conus lividus

<220>

<221> CDS

<222> (1)...(126)

<400> 333

gca ttt gat ggc agg aat gct gca gcc agc gac aaa gcg tcc gag ctg 48
 Ala Phe Asp Gly Arg Asn Ala Ala Ala Ser Asp Lys Ala Ser Glu Leu
 1 5 10 15

atg gct ctg gcc gtc agg gga tgc tgt tcc cat cct gcc tgt gct ggg 96
 Met Ala Leu Ala Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly
 20 25 30

agt aat gca cat atc tgt ggc aga aga cgc tgatgctcca ggaccctctg 146
 Ser Asn Ala His Ile Cys Gly Arg Arg Arg
 35 40

aaccacgacgt t 157

<210> 334

<211> 42

<212> PRT

<213> Conus lividus

<400> 334

Ala Phe Asp Gly Arg Asn Ala Ala Ala Ser Asp Lys Ala Ser Glu Leu
 1 5 10 15

Met Ala Leu Ala Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly
 20 25 30

Ser Asn Ala His Ile Cys Gly Arg Arg Arg
 35 40

<210> 335
 <211> 157
 <212> DNA
 <213> Conus lividus

<220>
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 <222> (1)..(117)

<400> 335
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 Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 1 5 10 15

aag ctg acc gtc agg gag gat tgc tgt tca gac cct cgc tgt tcc gtg 96
 Lys Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val
 20 25 30

gga cat caa gac atg tgt ggc tgaagacgct gatgctccag gaccctctga 147
 Gly His Gln Asp Met Cys Gly
 35

atcacgacgt 157

<210> 336
 <211> 39
 <212> PRT
 <213> Conus lividus

<400> 336
 Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 1 5 10 15

Lys Leu Thr Val Arg Glu Asp Cys Cys Ser Asp Pro Arg Cys Ser Val
 20 25 30

Gly His Gln Asp Met Cys Gly
 35

<210> 337
 <211> 154
 <212> DNA
 <213> Conus lividus

<220>
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 <222> (1)..(114)

<400> 337
 ttt gaa tgc agg aat gct gca ggc aac gac aaa gcg act gac ctg atg 48
 Phe Glu Cys Arg Asn Ala Ala Gly Asn Asp Lys Ala Thr Asp Leu Met
 1 5 10 15

gct ctg act gtc agg gga tgc tgt tcc cat cct gcc tgt gct ggg aat 96
 Ala Leu Thr Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn
 20 25 30

aat cca cat atc tgc ggc tgaagacgct gatgctccag gaccctctga 144
 Asn Pro His Ile Cys Gly
 35

119

accacgacgt 154

<210> 338
<211> 38
<212> PRT
<213> Conus lividus

<400> 338
Phe Glu Cys Arg Asn Ala Ala Gly Asn Asp Lys Ala Thr Asp Leu Met
1 5 10 15
Ala Leu Thr Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn
20 25 30
Asn Pro His Ile Cys Gly
35

<210> 339
<211> 154
<212> DNA
<213> Conus lividus

<220>
<221> CDS
<222> (1)...(114)

<400> 339
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Phe Asp Gly Arg Asn Ala Ala Asn Asn Lys Ala Thr Asp Leu Met
1 5 10 15
gct ctg act gtc aga gga tgc tgt ggc aat cct tca tgt agc atc cat 96
Ala Leu Thr Val Arg Gly Cys Cys Gly Asn Pro Ser Cys Ser Ile His
20 25 30
att cct tac gtt tgt aat tagagacact gatgctccag gaccctctga 144
Ile Pro Tyr Val Cys Asn
35

accacgacgt 154

<210> 340
<211> 38
<212> PRT
<213> Conus lividus

<400> 340
Phe Asp Gly Arg Asn Ala Ala Asn Asn Lys Ala Thr Asp Leu Met
1 5 10 15
Ala Leu Thr Val Arg Gly Cys Cys Gly Asn Pro Ser Cys Ser Ile His
20 25 30
Ile Pro Tyr Val Cys Asn
35

<210> 341
<211> 157
<212> DNA
<213> Conus lividus

120

<220>
<221> CDS
<222> (1)..(126)

<400> 341
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Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met
 1 5 10 15

aag cggtacc gac agc gaa gaa tgc 'tgt tta gac tct cgc tgt gcc ggg 96
Lys Arg Thr Asp Ser Glu Glu Cys Cys Leu Asp Ser Arg Cys Ala Gly
 20 25 30

caa cat caa gac ctg tgt ggc gga aga cgc tgatgctcca ggaccctctg 146
Gln His Gln Asp Leu Cys Gly Gly Arg Arg
 35 40

aaccacgacgt t 157

<210> 342
<211> 42
<212> PRT
<213> Conus lividus

<400> 342
Ser Asn Gly Arg Asn Ala Ala Ala Lys Phe Lys Ala Pro Ala Leu Met 48
 1 5 10 15

Lys Arg Thr Asp Ser Glu Glu Cys Cys Leu Asp Ser Arg Cys Ala Gly
 20 25 30

Gln His Gln Asp Leu Cys Gly Gly Arg Arg
 35 40

<210> 343
<211> 126
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (1)..(123)

<400> 343
tct gat ggc agg aat gcc gca gaa aag gac aaa gcg tct gac ctg gtc 48
Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
 1 5 10 15

gct ctg acc gtc aag gga tgc tgt tct aat cct ccc tgt tac gcg aat 96
Ala Leu Thr Val Lys Gly Cys Cys Ser Asn Pro Pro Cys Tyr Ala Asn
 20 25 30

aat caa gcc tat tgt aat gga aga cgc tga 126
Asn Gln Ala Tyr Cys Asn Gly Arg Arg
 35 40

<210> 344
<211> 41
<212> PRT
<213> Conus marmoreus

121

<400> 344
Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
1 5 10 15
Ala Leu Thr Val Lys Gly Cys Cys Ser Asn Pro Pro Cys Tyr Ala Asn
20 25 30
Asn Gln Ala Tyr Cys Asn Gly Arg Arg
35 40

<210> 345
<211> 117
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (1)..(114)

<400> 345
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Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
1 5 10 15
gct ctg acc gtc aag gga tgc tgt tct cat cct gcc tgt agc gtg aat 96
Ala Leu Thr Val Lys Gly Cys Cys Ser His Pro Ala Cys Ser Val Asn
20 25 30
aat cca gac att tgt ggt tga 117
Asn Pro Asp Ile Cys Gly
35

<210> 346
<211> 38
<212> PRT
<213> Conus marmoreus

<400> 346
Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp Lys Ala Ser Asp Leu Val
1 5 10 15
Ala Leu Thr Val Lys Gly Cys Cys Ser His Pro Ala Cys Ser Val Asn
20 25 30
Asn Pro Asp Ile Cys Gly
35

<210> 347
<211> 145
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)..(114)

<400> 347
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Ser Asp Gly Arg Asn Ala Ala Ala Asn Asn Lys Val Ala Leu Thr Met
1 5 10 15

122

agg gga aaa tgc tgt atc aat gat gcg tgt cgc tcg aaa cat cca cag 96
 Arg Gly Lys Cys Cys Ile Asn Asp Ala Cys Arg Ser Lys His Pro Gln
 20 25 30

tac tgt tct gga aga cgc tgatactcca ggaccctctg aaccacgacg t 145
 Tyr Cys Ser Gly Arg Arg
 35

<210> 348
<211> 38
<212> PRT
<213> Conus musicus

<400> 348
Ser Asp Gly Arg Asn Ala Ala Asn Asn Lys Val Ala Leu Thr Met
 1 5 10 15

Arg Gly Lys Cys Cys Ile Asn Asp Ala Cys Arg Ser Lys His Pro Gln
 20 25 30

Tyr Cys Ser Gly Arg Arg
 35

<210> 349
<211> 154
<212> DNA
<213> Conus musicus

<220>
<221> CDS
<222> (1)...(123)

<400> 349
tct gat ggc agg aat gct gca gcc aac gac aaa gtg tct gac cag atg 48
Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Val Ser Asp Gln Met
 1 5 10 15

gct ctg gtt gtc agg gga tgc tgt tac aat att gcc tgt aga att aat 96
Ala Leu Val Val Arg Gly Cys Cys Tyr Asn Ile Ala Cys Arg Ile Asn
 20 25 30

aat cca cgg tac tgt cgt gga aaa cgc tgatgttcca ggaccctctg 143
Asn Pro Arg Tyr Cys Arg Gly Lys Arg
 35 40

aaccacgacg t 154

<210> 350
<211> 41
<212> PRT
<213> Conus musicus

<400> 350
Ser Asp Gly Arg Asn Ala Ala Asn Asp Lys Val Ser Asp Gln Met
 1 5 10 15

Ala Leu Val Val Arg Gly Cys Cys Tyr Asn Ile Ala Cys Arg Ile Asn
 20 25 30

Asn Pro Arg Tyr Cys Arg Gly Lys Arg
 35 40

<210> 351
<211> 154
<212> DNA
<213> Conus obscurus

<220>
<221> CDS
<222> (52)..(123)

<400> 351
tctgaaggca ggaatgccgc agccaacgac aaagcgctcg acctgatggc t ctg aac 57
Leu Asn
1

gtc agg gga tgc tgt tcc cat cct gtc tgt cgc ttc aat tat cca aaa 105
Val Arg Gly Cys Cys Ser His Pro Val Cys Arg Phe Asn Tyr Pro Lys
5 10 15

tat tgt ggt gga aga cgc tgatggtcca ggaccctctg aaccacgacg t 154
Tyr Cys Gly Gly Arg Arg
20

<210> 352
<211> 24
<212> PRT
<213> Conus obscurus

<400> 352
Leu Asn Val Arg Gly Cys Cys Ser His Pro Val Cys Arg Phe Asn Tyr
1 5 10 15

Pro Lys Tyr Cys Gly Gly Arg Arg
20

<210> 353
<211> 151
<212> DNA
<213> Conus obscurus

<220>
<221> CDS
<222> (46)..(111)

<400> 353
tctgatggcg ggaatgccgc agcaaaagcg tttgatctaa tcact ctg gcc ctc agg 57
Leu Ala Leu Arg
1

gat gaa tgc tgt gcc agt cct ccc tgt cgt ttg aat aat cca tac gta 105
Asp Glu Cys Cys Ala Ser Pro Pro Cys Arg Leu Asn Asn Pro Tyr Val
5 10 15 20

tgt cat tgacgacgct gatgctccag gaccctctga accacgacgt 151
Cys His

<210> 354
<211> 22
<212> PRT
<213> Conus obscurus

124

<400> 354
 Leu Ala Leu Arg Asp Glu Cys Cys Ala Ser Pro Pro Cys Arg Leu Asn
 1 5 10 15
 Asn Pro Tyr Val Cys His
 20

<210> 355
 <211> 217
 <212> DNA
 <213> Conus obscurus

<220>
 <221> CDS
 <222> (1)..(186)

<400> 355
 atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 ccc act tca gat cgt gca tct gat agg agg aat gcc gca gcc aaa gcg 96
 Pro Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Ala Lys Ala
 20 25 30
 ttt gac ctg aga tat tcg acc gcc aag aga gga tgc tgt tcc aat cct 144
 Phe Asp Leu Arg Tyr Ser Thr Ala Lys Arg Gly Cys Cys Ser Asn Pro
 35 40 45
 gtc tgt tgg cag aat aat gca gaa tac tgt cgt gaa agt ggc 186
 Val Cys Trp Gln Asn Asn Ala Glu Tyr Cys Arg Glu Ser Gly
 50 55 60
 taatgctcca ggaccctctg aaccacgacg t 217

<210> 356
 <211> 62
 <212> PRT
 <213> Conus obscurus

<400> 356
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser 48
 1 5 10 15
 Pro Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Ala Lys Ala
 20 25 30
 Phe Asp Leu Arg Tyr Ser Thr Ala Lys Arg Gly Cys Cys Ser Asn Pro
 35 40 45
 Val Cys Trp Gln Asn Asn Ala Glu Tyr Cys Arg Glu Ser Gly 186
 50 55 60

<210> 357
 <211> 208
 <212> DNA
 <213> Conus obscurus

<220>
 <221> CDS
 <222> (1)..(168)

125

<400> 357
atg ttc acc gtg ttt ctg ttg gtc ttg gca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
ttc act tca gat cgt gca tct gat ggc ggg aat gtc gca gcg tct cac 96
Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Val Ala Ala Ser His
20 25 30
ctg atc gct ctg acc atc aag gga tgc tgt tct cac cct ccc tgt gcc 144
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala
35 40 45
cag aat aat caa gac tat tgt ggt tgacgacgct gatgctccag gaccctctga 198
Gln Asn Asn Gln Asp Tyr Cys Gly
50 55
accacgacgt 208

<210> 358
<211> 56
<212> PRT
<213> Conus obscurus
<400> 358
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Phe Thr Ser Asp Arg Ala Ser Asp Gly Gly Asn Val Ala Ala Ser His
20 25 30
Leu Ile Ala Leu Thr Ile Lys Gly Cys Cys Ser His Pro Pro Cys Ala
35 40 45
Gln Asn Asn Gln Asp Tyr Cys Gly
50 55

<210> 359
<211> 217
<212> DNA
<213> Conus obscurus
<220>
<221> CDS
<222> (1)...(186)
<400> 359
atg ttc acc gtg ttt ctg ttg gtc tta tca acc acc gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ser Thr Thr Val Val Ser
1 5 10 15
tcc act tca gat cgt gca tct gat agg agg aat gcc gca gcc aaa gcg 96
Ser Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Lys Ala
20 25 30
tct gac ctg atg tat tcg acc gtc aag aaa gga tgt tgt tcc cat cct 144
Ser Asp Leu Met Tyr Ser Thr Val Lys Lys Gly Cys Cys Ser His Pro
35 40 45
gcc tgt tcg ggg aat aat cga gaa tat tgt cgt gaa agt ggc 186
Ala Cys Ser Gly Asn Asn Arg Glu Tyr Cys Arg Glu Ser Gly
50 55 60

126

taatgctcca ggaccctctg aaccacgacg t 217

<210> 360
<211> 62
<212> PRT
<213> Conus obscurus

<400> 360
Met Phe Thr Val Phe Leu Leu Val Val Leu Ser Thr Thr Val Val Ser
1 5 10 15

Ser Thr Ser Asp Arg Ala Ser Asp Arg Arg Asn Ala Ala Ala Lys Ala
20 25 30

Ser Asp Leu Met Tyr Ser Thr Val Lys Lys Gly Cys Cys Ser His Pro
35 40 45

Ala Cys Ser Gly Asn Asn Arg Glu Tyr Cys Arg Glu Ser Gly
50 55 60

<210> 361
<211> 157
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (52)..(126)

<400> 361
tttcatggca ggaatgcctc agccgacagc aaagtggctg cccggatcgc t cag atc 57
Gln Ile
1

gac agg gat cca tgc tgt tcc tat cct gac tgt ggc gcg aat cat cca 105
Asp Arg Asp Pro Cys Cys Ser Tyr Pro Asp Cys Gly Ala Asn His Pro
5 10 15

gag att tgt ggt gga aaa cgc tgatgctcca ggaccctctg aaccacgacg t 157
Glu Ile Cys Gly Gly Lys Arg
20 25

<210> 362
<211> 25
<212> PRT
<213> Conus omaria

<400> 362
Gln Ile Asp Arg Asp Pro Cys Cys Ser Tyr Pro Asp Cys Gly Ala Asn
1 5 10 15

His Pro Glu Ile Cys Gly Gly Lys Arg
20 25

<210> 363
<211> 128
<212> DNA
<213> Conus omaria

<220>

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127

<221> CDS
 <222> (26) .. (88)

<400> 363
 tctcatggca ggaatgccgc acgct ctg acc gtc agg gaa tgc tgt tct cag 52
 Leu Thr Val Arg Glu Cys Cys Ser Gln
 1 5

cct cct tgt cgc tgg aaa cat cca gaa ctt tgt agt tgaagacgct 98
 Pro Pro Cys Arg Trp Lys His Pro Glu Leu Cys Ser
 10 15 20

gatgctccag gaccctctga accacgacgt 128

<210> 364
 <211> 21
 <212> PRT
 <213> Conus omaria

<400> 364
 Leu Thr Val Arg Glu Cys Cys Ser Gln Pro Pro Cys Arg Trp Lys His
 1 5 10 15
 Pro Glu Leu Cys Ser
 20

<210> 365
 <211> 154
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (52) .. (123)

<400> 365
 tttgatggca ggaatgctgc agccagcgac aaagcgtctg agctgatggc t ctg gcc 57
 Leu Ala
 1

gtc agg gga tgc tgt tcc cat cct gcc tgt gct ggg aat aat cca cat 105
 Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn Asn Pro His
 5 10 15

atc tgt ggc aga aga cgc tgatgctcca ggaccctctg aaccacgacg t 154
 Ile Cys Gly Arg Arg Arg
 20

<210> 366
 <211> 24
 <212> PRT
 <213> Conus omaria

<400> 366
 Leu Ala Val Arg Gly Cys Cys Ser His Pro Ala Cys Ala Gly Asn Asn
 1 5 10 15
 Pro His Ile Cys Gly Arg Arg Arg
 20

WO 00/44776

128

<210> 367
<211> 142
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (40)..(102)

<400> 367
tctggtgtca ggaaagacgc agcgccctggc ctgatcgct ctg acc atc aag gga 54
Leu Thr Ile Lys Gly
1 5

tgc tgt tct gat cct agc tgt aac gtg aat aat cca gac tat tgt ggt 102
Cys Cys Ser Asp Pro Ser Cys Asn Val Asn Asn Pro Asp Tyr Cys Gly
10 15 20

tgacgacgct gatgctccag gaccctctga accacgacgt 142

<210> 368
<211> 21
<212> PRT
<213> Conus omaria

<400> 368
Leu Thr Ile Lys Gly Cys Cys Ser Asp Pro Ser Cys Asn Val Asn Asn 1 5 10 15
Pro Asp Tyr Cys Gly 20

<210> 369
<211> 157
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (52)..(117)

<400> 369
tctaattggca ggaatgccgc agccaaattc aaagcgccctg ccctgatgga g ctg acc 57
Leu Thr
1

gtc agg gaa gaa tgc tgt tca gac cct cgc tgt tcc gtg gga cat caa 105
Val Arg Glu Glu Cys Cys Ser Asp Pro Arg Cys Ser Val Gly His Gln
5 10 15

gat atg tgt cgg tgaagcacgt gatgctccag gaccctctga accacgacgt 157
Asp Met Cys Arg 20

<210> 370
<211> 22
<212> PRT
<213> Conus omaria

<400> 370
Leu Thr Val Arg Glu Glu Cys Cys Ser Asp Pro Arg Cys Ser Val Gly

129

1	5	10	15
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His Gln Asp Met Cys Arg
20

<210> 371
<211> 151
<212> DNA
<213> <i>Conus purpurascens</i>

<220>
<221> CDS
<222> (1)...(120)

<400> 371
act gat ggc agg aat gct gca gcc ata gcg ctt gac ctg atc gct ccg 48
Thr Asp Gly Arg Asn Ala Ala Ala Ile Ala Leu Asp Leu Ile Ala Pro
1 5 10 15

gcc gtc agg gga gga tgc tgt tcc aat cct gcc tgt tta gtg aat cat 96
Ala Val Arg Gly Gly Cys Cys Ser Asn Pro Ala Cys Leu Val Asn His
20 25 30

cta gaa atg tgt ggt aaa aga cgc tgatccccca ggaccctctg aaccacgacg 150
Leu Glu Met Cys Gly Lys Arg Arg
35 40

t
151

<210> 372
<211> 40
<212> PRT
<213> <i>Conus purpurascens</i>

<400> 372
Thr Asp Gly Arg Asn Ala Ala Ala Ile Ala Leu Asp Leu Ile Ala Pro
1 5 10 15

Ala Val Arg Gly Gly Cys Cys Ser Asn Pro Ala Cys Leu Val Asn His
20 25 30

Leu Glu Met Cys Gly Lys Arg Arg
35 40

<210> 373
<211> 160
<212> DNA
<213> <i>Conus purpurascens</i>

<220>
<221> CDS
<222> (1)...(120)

<400> 373
tct gat ggc agg gat gcc gca gcc aac gac aaa gcg tct gac ctg atc 48
Ser Asp Gly Arg Asp Ala Ala Ala Asn Asp Lys Ala Ser Asp Leu Ile
1 5 10 15

gct ctg acc gcc agg aga gat cca tgc tgt ttc aat cct gcc tgt aac 96
Ala Leu Thr Ala Arg Arg Asp Pro Cys Cys Phe Asn Pro Ala Cys Asn
20 25 30

130

gtg aat aat cca cag att tgt ggt tgaagacgct gatgctccag gaccctctga 150
Val Asn Asn Pro Gln Ile Cys Gly
35 40

accacacgat 160

<210> 374
<211> 40
<212> PRT
<213> Conus purpurascens

<400> 374
Ser Asp Gly Arg Asp Ala Ala Asn Asp Lys Ala Ser Asp Leu Ile
1 5 10 15

Ala Leu Thr Ala Arg Arg Asp Pro Cys Cys Phe Asn Pro Ala Cys Asn
20 25 30

Val Asn Asn Pro Gln Ile Cys Gly
35 40

<210> 375
<211> 151
<212> DNA
<213> Conus purpurascens

<220>
<221> CDS
<222> (1)..(120)

<400> 375
tct gat ggc agg gat gct gag aaa aca ggc ttt gac acg acc att gtg 48
Ser Asp Gly Arg Asp Ala Glu Lys Thr Gly Phe Asp Thr Thr Ile Val
1 5 10 15

ccg gaa gac tgc tgt tcg gat cct tcc tgt tgg agg ctg cat agt tta 96
Pro Glu Asp Cys Cys Ser Asp Pro Ser Cys Trp Arg Leu His Ser Leu
20 25 30

gct tgt act gga att gta aac cgc tgatgctcca ggaccctctg aaccacgacg 150
Ala Cys Thr Gly Ile Val Asn Arg
35 40

t 151

<210> 376
<211> 40
<212> PRT
<213> Conus purpurascens

<400> 376
Ser Asp Gly Arg Asp Ala Glu Lys Thr Gly Phe Asp Thr Thr Ile Val
1 5 10 15

Pro Glu Asp Cys Cys Ser Asp Pro Ser Cys Trp Arg Leu His Ser Leu
20 25 30

Ala Cys Thr Gly Ile Val Asn Arg
35 40

<210> 377
 <211> 142
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (1)..(111)

<400> 377

act	gat	ggc	agg	agt	gct	gca	gcc	ata	gcg	ttt	gcc	ctg	atc	gct	ccg	48
Thr	Asp	Gly	Arg	Ser	Ala	Ala	Ala	Ile	Ala	Phe	Ala	Leu	Ile	Ala	Pro	
1				5					10					15		

acc gtc tgc tgt act aat cct gcc tgt ctc gtg aat aat ata cgc ttt
 Thr Val Cys Cys Thr Asn Pro Ala Cys Leu Val Asn Asn Ile Arg Phe
 20 25 30 96

tgt ggt gga aga cgc tgatgccccca ggaccctctg aaccacgacg t
 Cys Gly Gly Arg Arg
 35 142

<210> 378
 <211> 37
 <212> PRT
 <213> Conus purpurascens

<400> 378

Thr	Asp	Gly	Arg	Ser	Ala	Ala	Ala	Ile	Ala	Phe	Ala	Leu	Ile	Ala	Pro	48
1				5					10					15		

Thr Val Cys Cys Thr Asn Pro Ala Cys Leu Val Asn Asn Ile Arg Phe
 20 25 30

Cys Gly Gly Arg Arg
 35

<210> 379
 <211> 157
 <212> DNA
 <213> Conus regius

<220>
 <221> CDS
 <222> (1)..(117)

<400> 379

tct	gat	gga	aga	aat	gcc	gca	agc	gac	gcc	aaa	gcg	ttt	ccc	cgg	atc	48
Ser	Asp	Gly	Arg	Asn	Ala	Ala	Ser	Asp	Ala	Lys	Ala	Phe	Pro	Arg	Ile	
1					5					10				15		

gct cca atc gtc agg gac gaa tgc tgt agc gat cct agg tgt cac ggg
 Ala Pro Ile Val Arg Asp Glu Cys Cys Ser Asp Pro Arg Cys His Gly
 20 25 30 96

aat aat cgg gac cac tgt gct tgaagacgct gctgctccag gaccctctga
 Asn Asn Arg Asp His Cys Ala
 35 147

accacgacgat 157

132

<210> 380

<211> 39

<212> PRT

<213> Conus regius

<400> 380

Ser	Asp	Gly	Arg	Asn	Ala	Ala	Ser	Asp	Ala	Lys	Ala	Phe	Pro	Arg	Ile
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Ala	Pro	Ile	Val	Arg	Asp	Glu	Cys	Cys	Ser	Asp	Pro	Arg	Cys	His	Gly
			20				25						30		

Asn	Asn	Arg	Asp	His	Cys	Ala
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<222> (1)...(117)

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1					5				10					15	

tct	caa	act	gtc	aag	aga	gat	tgc	tgt	tcc	cat	cct	ctc	tgt	aga	tta
Ser	Gln	Thr	Val	Lys	Arg	Asp	Cys	Cys	Ser	His	Pro	Leu	Cys	Arg	Leu
			20				25						30		

ttt	gtt	cca	gga	ctt	tgt	att	tgaagacgt	gctgctccag	gaccctctga						147
Phe	Val	Pro	Gly	Leu	Cys	Ile									
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156

<210> 382

<211> 39

<212> PRT

<213> Conus regius

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Ser	Gln	Thr	Val	Lys	Arg	Asp	Cys	Cys	Ser	His	Pro	Leu	Cys	Arg	Leu
			20				25						30		

Phe	Val	Pro	Gly	Leu	Cys	Ile
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<211> 157

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133

<222> (1) .. (117)

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gct caa atc gtc agg aga gga tgc tgt tcc cat cct gtc tgt aaa gtg 96
 Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Val Cys Lys Val
 20 25 30

agg tat cca gac ctg tgt cgt tgaagacgct gctgctccag gaccctctga 147
Arg Tyr Pro Asp Leu Cys Arg
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accacgacgt 157

<210> 384

<211> 39

<212> PRT

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<400> 384

Ser Asp Gly Arg Asn Ala Ala Ala Asp Asn Lys Ala Ser Asp Leu Ile
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Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Val Cys Lys Val
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Arg Tyr Pro Asp Leu Cys Arg
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<222> (1)..(117)

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gct caa atc gtc agg aga gga tgc tgt tcc cat cct gcc tgt aat gtg 96
Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Ala Cys Asn Val
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aat aat cca cac att tgt ggt tgaagacgct gctgctccag gaccctctga 14/
Asn Asn Pro His Ile Cys Gly
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accacgacgt 157

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212 PRI
213 Con

213 Cor

134

<400> 386
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 Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Ala Cys Asn Val
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 Ala Gln Ile Val Arg Arg Gly Cys Cys Ser His Pro Val Cys Lys Val
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 Arg Tyr Ser Asp Met Cys Gly
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 20 25 30
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 <222> (1)..(114)

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135

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Phe Pro His Ser Cys Gly				
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cac cag gta tgc tgt tcc aac cct gtc tgt cac gtg gat cat cca gaa				96
His Gln Val Cys Cys Ser Asn Pro Val Cys His Val Asp His Pro Glu				
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ctt tgt cgt aga aga cgc tgatgctcca ggaccctctg aaccacgacg t				145
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1 5 10 15

gct ccg gcc atc agg gga tgc tgt tcc cac cct gtc tgt aac ttg agt 96
Ala Pro Ala Ile Arg Gly Cys Cys Ser His Pro Val Cys Asn Leu Ser
20 25 30

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Asn Pro Gln Ile Cys Arg Gly Arg Arg
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1 5 10 15

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cat cca gaa att tgt cgt tga 117

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Ile Arg Phe Cys Gly Gly Arg Arg
35 40

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1					5				10					15			

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					20				25				30				

<400> 400

aat	aat	cca	ggc	ctt	tgc	act	tgaagatgct	gctgccccag	gaccctctga							147
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accacgacgt

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					20				25			30					

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Ile Lys Ala Cys Val Phe
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gtc agg aga gga tgc tgt ggc aat cct gcc tgt agc ggc tcc tcg aaa 96
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accacgacgt 154

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<400> 404
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20 25 30

Asp Ala Pro Ser Cys Gly
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/01979

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C07K 14/00, 14/435, 7/08; A61K 38/10, 38/17

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350, 530/300, 530/326, 514/12, 514/13, 536/23.5, 514/2, 435/7.23, 436/64, 530/324, 514/21, 530/855

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN: BIOSIS, MEDLINE, SCISEARCH, USPAT, CAPLUS, BIOTECHDS, DGENE.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	US 5,866,682 A (MCINTOSH et al.) 02 February 1999 (02.02.99), see entire document.	1-39
Y	US 5,432,155 A (OLIVERA et al.) 11 July 1995 (11.07.95), see entire document.	1-9
Y	US 5,672,682 A (TERLAU et al.) 30 September 1997 (30.09.97), see entire document.	1-9
Y	US 5,595,972 A (OLIVERA et al.) 21 January 1997 (21.02.97), see entire document.	1-39
Y	US 5,719,264 A (SHON et al.) 17 February 1998 (17.02.98), see entire document.	1-39
Y,P	US 5,969,096 A (SHON et al.) 10 October 1999 (10.10.99), see entire document.	1-9

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"		document defining the general state of the art which is not considered to be of particular relevance
"B"	"X"	earlier document published on or after the international filing date
"L"		document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O"	"Y"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"P"	"A"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
		document member of the same patent family

Date of the actual completion of the international search

31 MAY 2000

Date of mailing of the international search report

13 JUL 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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Washington, D.C. 20231
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/01979

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,670,622 A (SHON et al.) 23 September 97 (23.09.97), see entire document.	1-9
A	US 5,739,276 A (SHON et al.) 14 April 98 (14.04.98), see entire document.	1-9
A,P	US 5,889,147 A (CRUZ et al.) 30 March 1999 (30.03.99), see entire reference.	1-9

INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US00/01979**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: 1-39 (in-part) because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claims 1-39 were searched only to the extent that no search of the sequences was conducted because the computer readable form of the sequence listing is defective.

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No. PCT/US00/01979

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

530/350, 530/300, 530/326, 514/12, 514/13, 536/23.5, 514/2, 435/7.23, 436/64, 530/324, 514/21, 530/855.